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OM protein - protein search, using sw model

Run on: November 24, 2002, 10:09:06 ; Search time 13.1116 Seconds
(without alignments)
527.349 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242
Sequence: 1 MTYVAPAMSPPTTYLLLLLLL.....RPGQVPVPSPDQLLVEH 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 segs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCrus.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	1	US-08-243-545-6
2	1242	100.0	235	2	US-08-993-962-6
3	1242	100.0	235	4	US-09-160-841-6
4	1242	100.0	235	4	US-09-109-100-1
5	1242	100.0	235	5	PCT-US94-05365-6
6	1124	90.5	212	4	US-09-109-100-10
7	1114	89.7	209	4	US-09-109-100-18
8	1110	89.4	209	4	US-09-109-100-9
9	1110	89.4	209	4	US-09-109-100-12
10	1110	89.4	209	4	US-09-109-100-14
11	1110	89.4	209	4	US-09-109-100-17
12	1108	89.2	209	4	US-09-109-100-11
13	1108	89.2	209	4	US-09-109-100-15
14	1107	89.1	209	4	US-09-109-100-13
15	1106	89.0	209	4	US-09-109-100-8
16	1100	88.6	209	4	US-09-109-100-16
17	768.5	61.9	231	1	US-08-243-545-2
18	768.5	61.9	231	2	US-08-993-962-2
19	768.5	61.9	231	4	US-09-160-841-2
20	768.5	61.9	231	5	PCT-US94-05365-2
21	765.5	61.6	231	1	US-08-220-379B-7
22	765.5	61.6	231	1	PCT-US95-03866-6
23	506.5	40.8	137	4	US-09-109-100-19
24	154	12.4	42	5	PCT-US94-05150-17
25	91.5	7.4	675	1	US-08-317-522A-9
26	91.5	7.4	675	1	US-08-439-818A-9
27	91.5	7.4	675	2	US-08-751-965-9

28	91.5	7.4	675	2	US-08-738-975-9	Sequence 9, Appli
29	91.5	7.4	675	3	US-08-728-626-9	Sequence 9, Appli
30	91.5	7.4	675	2	US-08-808-599A-9	Sequence 9, Appli
31	87.5	7.0	415	4	US-09-006-353A-6	Sequence 6, Appli
32	87.5	7.0	415	4	US-09-573-986-6	Sequence 6, Appli
33	85	6.8	366	1	US-08-004-492-8	Sequence 8, Appli
34	84.5	6.8	913	1	US-08-445-640-4	Sequence 4, Appli
35	84.5	6.8	913	3	US-08-170-558-4	Sequence 4, Appli
36	84.5	6.8	913	3	US-08-447-314-4	Sequence 4, Appli
37	84.5	6.8	913	3	US-08-445-461-4	Sequence 4, Appli
38	84	6.8	107	4	US-09-220-528-52	Sequence 52, Appli
39	84	6.8	220	4	US-09-220-528-26	Sequence 26, Appli
40	83.5	6.7	429	1	US-07-964-589-2	Sequence 2, Appli
41	83.5	6.7	429	5	PCT-US93-02024-2	Sequence 2, Appli
42	83.5	6.7	671	3	US-09-121-321-16	Sequence 16, Appli
43	83.5	6.7	671	4	US-08-933-803A-16	Sequence 16, Appli
44	83	6.7	28	5	PCT-US94-05150-12	Sequence 12, Appli
45	83	6.7	758	1	US-07-756-250-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1
US-08-243-545-6
; Sequence 6, Application US/08243545
; Patent No. 5554512
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for fli3/Fli-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,545
FILING DATE: 11-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 387-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-243-545-6

Query Match 100.0%; Score 1242; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLSSGSLSGTQDCSFQHSPISSDPAVKIRLSYLLQDYVTV 60
Db 1 MTVALPAMSPPTTYLLLLSSGSLSGTQDCSFQHSPISSDPAVKIRLSYLLQDYVTV 60
QY 61 ASNLODEELCGIMRLVLAQRMMERLKTAVAGSKMOGLLERVNTEIHFTVKCAFQPPSCL 120
Db 61 ASNLODEELCGIMRLVLAQRMMERLKTAVAGSKMOGLLERVNTEIHFTVKCAFQPPSCL 120
QY 121 RRVQTNISRLLOETSEQLVALKPWITTRONFSRCLELQCPDSSSTLPPMSPRPLEATAPT 180
Db 121 RRVQTNISRLLOETSEQLVALKPWITTRONFSRCLELQCPDSSSTLPPMSPRPLEATAPT 180
QY 181 APQPLLILLLLPYGLLLAAACLIHMQRTRRRPRREGVPPVPSFODLLVHEH 235
Db 181 APQPLLILLLLPYGLLLAAACLIHMQRTRRRPRREGVPPVPSFODLLVHEH 235

RESULT 2

US-08-993-962-6
Sequence 6, Application US/08993962
Patent No. 5843423

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,962
FILING DATE: December 18, 1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-993-962-6

Query Match 100.0%; Score 1242; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLSSGSLSGTQDCSFQHSPISSDPAVKIRLSYLLQDYVTV 60
Db 1 MTVALPAMSPPTTYLLLLSSGSLSGTQDCSFQHSPISSDPAVKIRLSYLLQDYVTV 60
QY 61 ASNLODEELCGIMRLVLAQRMMERLKTAVAGSKMOGLLERVNTEIHFTVKCAFQPPSCL 120
Db 61 ASNLODEELCGIMRLVLAQRMMERLKTAVAGSKMOGLLERVNTEIHFTVKCAFQPPSCL 120
QY 121 RRVQTNISRLLOETSEQLVALKPWITTRONFSRCLELQCPDSSSTLPPMSPRPLEATAPT 180
Db 121 RRVQTNISRLLOETSEQLVALKPWITTRONFSRCLELQCPDSSSTLPPMSPRPLEATAPT 180
QY 181 APQPLLILLLLPYGLLLAAACLIHMQRTRRRPRREGVPPVPSFODLLVHEH 235
Db 181 APQPLLILLLLPYGLLLAAACLIHMQRTRRRPRREGVPPVPSFODLLVHEH 235

RESULT 3

US-09-160-841-6
Sequence 6, Application US/09160841
Patent No. 6190655

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,841
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 235 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-160-841-6

Query Match      100.0%; Score 1242; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDFAVKIRLSYLLQDYPVTV 60
    |||||||
Db 1 MTVLAPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDFAVKIRLSYLLQDYPVTV 60

QY 61 ASNLODEELCGIMRLVLAQRMERLKTIVAGSKMOGLLEERVNTEIHFVTKCAQPPPSCL 120
    |||||||
Db 61 ASNLODEELCGIMRLVLAQRMERLKTIVAGSKMOGLLEERVNTEIHFVTKCAQPPPSCL 120

QY 121 REVQTNISRLQETSEQLVALKPWITRONFSRCLELOCQPDSSITLPPWSPRPLEATAPT 180
    |||||||
Db 121 REVQTNISRLQETSEQLVALKPWITRONFSRCLELOCQPDSSITLPPWSPRPLEATAPT 180

QY 181 APQPLLLLLLPVGLLLAAAMCLHMQRTRRTPRPGEOVPVPSPQDILLVEH 235
    |||||||
Db 181 APQPLLLLLLPVGLLLAAAMCLHMQRTRRTPRPGEOVPVPSPQDILLVEH 235

RESULT 4
US-09-109-100-1
; Sequence 1, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-1

Query Match      100.0%; Score 1242; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDFAVKIRLSYLLQDYPVTV 60
    |||||||
Db 1 MTVLAPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDFAVKIRLSYLLQDYPVTV 60

QY 61 ASNLODEELCGIMRLVLAQRMERLKTIVAGSKMOGLLEERVNTEIHFVTKCAQPPPSCL 120
    |||||||
Db 61 ASNLODEELCGIMRLVLAQRMERLKTIVAGSKMOGLLEERVNTEIHFVTKCAQPPPSCL 120

QY 121 REVQTNISRLQETSEQLVALKPWITRONFSRCLELOCQPDSSITLPPWSPRPLEATAPT 180
    |||||||
Db 121 REVQTNISRLQETSEQLVALKPWITRONFSRCLELOCQPDSSITLPPWSPRPLEATAPT 180

QY 181 APQPLLLLLLPVGLLLAAAMCLHMQRTRRTPRPGEOVPVPSPQDILLVEH 235
    |||||||
Db 181 APQPLLLLLLPVGLLLAAAMCLHMQRTRRTPRPGEOVPVPSPQDILLVEH 235

RESULT 5
PCT-US94-05365-6
; Sequence 6, Application PC/TUS9405365
; GENERAL INFORMATION:
```

```
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05365
; FILING DATE: May 24, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: -to be assigned-
; FILING DATE: May 11, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,502
; FILING DATE: March 7, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/162,407
; FILING DATE: December 3, 1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 235 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-05365-6

Query Match      100.0%; Score 1242; DB 5; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDFAVKIRLSYLLQDYPVTV 60
    |||||||
Db 1 MTVLAPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDFAVKIRLSYLLQDYPVTV 60

QY 61 ASNLODEELCGIMRLVLAQRMERLKTIVAGSKMOGLLEERVNTEIHFVTKCAQPPPSCL 120
    |||||||
Db 61 ASNLODEELCGIMRLVLAQRMERLKTIVAGSKMOGLLEERVNTEIHFVTKCAQPPPSCL 120

QY 121 REVQTNISRLQETSEQLVALKPWITRONFSRCLELOCQPDSSITLPPWSPRPLEATAPT 180
    |||||||
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Db 121 RFVQINISRLQETSEQVIAKLPMTITRQNSRCLQOCQPPSSSTLPPWSPRLPLEATAPT 180
QY 181 APQPLLLLLLPGVGLLLAAACLMHQRTRRRTPRGEQVPPVPSQDILLVEH 235
Db 181 APQPLLLLLLPGVGLLLAAACLMHQRTRRRTPRGEQVPPVPSQDILLVEH 235

RESULT 6

US-09-109-100-10
; Sequence 10, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-10

Query Match 90.5%; Score 1124; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.2e-105;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 SGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVAASNLQDEELCGIMRLVLAQRME 84
Db 2 SGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVAASNLQDEELCGIMRLVLAQRME 61
QY 85 RLKTVAGSKMOGLERVNTIEHFVTKCAFQPPSCLRFVQTNISRLQETSEQVIAKLPW 144
Db 62 RLKTVAGSKMOGLERVNTIEHFVTKCAFQPPSCLRFVQTNISRLQETSEQVIAKLPW 121
QY 145 ITRQNSRCLQOCQPPSSSTLPPWSPRLPLEATAPTAPQPLLLLLLPGVGLLLAAAC 204
Db 122 ITRQNSRCLQOCQPPSSSTLPPWSPRLPLEATAPTAPQPLLLLLLPGVGLLLAAAC 181
QY 205 LHMQRTRRRTPRGEQVPPVPSQDILLVEH 235
Db 182 LHMQRTRRRTPRGEQVPPVPSQDILLVEH 212

RESULT 7

US-09-109-100-18
; Sequence 18, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-18

Query Match 89.7%; Score 1114; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.2e-104;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVAASNLQDEELCGIMRLVLAQRME 86
Db 181 APQPLLLLLLPGVGLLLAAACLMHQRTRRRTPRGEQVPPVPSQDILLVEH 235

Db 1 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVAASNLQDEELCGIMRLVLAQRME 86
QY 87 KTVAGSKMOGLERVNTIEHFVTKCAFQPPSCLRFVQTNISRLQETSEQVIAKLPW 146
Db 61 KTVAGSKMOGLERVNTIEHFVTKCAFQPPSCLRFVQTNISRLQETSEQVIAKLPW 120
QY 147 ITRQNSRCLQOCQPPSSSTLPPWSPRLPLEATAPTAPQPLLLLLLPGVGLLLAAAC 206
Db 122 ITRQNSRCLQOCQPPSSSTLPPWSPRLPLEATAPTAPQPLLLLLLPGVGLLLAAAC 180
QY 207 WQTRRRTPRGEQVPPVPSQDILLVEH 235
Db 181 WQTRRRTPRGEQVPPVPSQDILLVEH 209

RESULT 8

US-09-109-100-9
; Sequence 9, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-9

Query Match 89.4%; Score 1110; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 3e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVAASNLQDEELCGIMRLVLAQRME 86
Db 1 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVAASNLQDEELCGIMRLVLAQRME 60
QY 87 KTVAGSKMOGLERVNTIEHFVTKCAFQPPSCLRFVQTNISRLQETSEQVIAKLPW 146
Db 61 KTVAGSKMOGLERVNTIEHFVTKCAFQPPSCLRFVQTNISRLQETSEQVIAKLPW 120
QY 147 ITRQNSRCLQOCQPPSSSTLPPWSPRLPLEATAPTAPQPLLLLLLPGVGLLLAAAC 206
Db 121 ITRQNSRCLQOCQPPSSSTLPPWSPRLPLEATAPTAPQPLLLLLLPGVGLLLAAAC 180
QY 207 WQTRRRTPRGEQVPPVPSQDILLVEH 235
Db 181 WQTRRRTPRGEQVPPVPSQDILLVEH 209

RESULT 9

US-09-109-100-12
; Sequence 12, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-12

Query Match 89.7%; Score 1114; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.2e-104;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match	89.4%;	Score 1110;	DB 4;	Length 209;
Best Local Similarity	99.5%;	Pred. No. 3e-104;		
Matches 208; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	27	TQDSHSPHISDDPAVXIRELSYLDQYPVYVANSIQDEELGGJMRVIAQRWBERL	86
Db	1	TQDSQHSHPISDDPAVXIRELSYFLQDYPVYVANSIQDEELGGJMRVIAQRWBERL	60
QY	87	KTYAGSKMGJLEERNTEIHEVTKCAFOPPSCJLRSVQTNISRLQENSEQJVALKPMIT	146
Db	61	KTYAGSKMGJLEERNTEIHEVTKCAFOPPSCJLRVQTNISRLQENSEQJVALKPMIT	120
QY	147	RQNFSCJELQCPDSSJLRPPWSPRLEATAPABQAPLLDLLLVGLLTLAAACJH	206
Db	121	RQNFSCJELQCPDSSJLRPPWSPRLEATAPABQAPLLDLLLVGLLTLAAACJH	180
QY	207	WQTRRRTRPRGEOVPPVPSQDILLVYEH	235
Db	181	WQTRRRTRPRGEOVPPVPSQDILLVYEH	209

RESULT 10-109-100-14
 US-09-109-100-14
 Sequence 14, Application US/09109100C
 Patent No. 6291661
 GENERAL INFORMATION:
 APPLICANT: Graddis, Thomas J.
 APPLICANT: McGrew, Jeffrey T.
 TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
 FILE REFERENCE: 03360, 0038
 CURRENT APPLICATION NUMBER: US/09/109,100C
 CURRENT FILING DATE: 1998-07-02
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 14
 LENGTH: 209
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-109-100-14

Query Match	89.48;	Score 1110;	DB 4;	Length 209;
Best Local Similarity	99.58;	Pred. No. 3e-104;		
Matches 208; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0

Qy	27	TQDCSQHPISSDPAVKIRLSTYLLQDIPVYASMLQDEELCGMLRVLAQRMERL	86
Db	1	TQDCSQHPISSDPAVKIRLSTYLLQDIPVYASMLQDEELCGMLRVLAQRMERL	60
Qy	87	KTVAGSMOGLLEERNTEHFTYCAQPPSCSLRFQNTISRLQETSEQVALKPIT	146
Db	61	KTVAGSMOGLLEERNTEHFTYCAQPPSCSLRFQNTISRLQETSEQVALKPIT	120
Qy	147	RQNFSRCLQCCQPSSTLPPWSBRPLEATAPAPQPLLLLLLPVGLLLAAAWCLH	206
Db	121	RQNFSRCLQCCQPSSTLPPWSBRPLEATAPAPQPLLLLLLPVGLLLAAAWCLH	186
Qy	207	WQTRRRTPRPGEQVPPVPSQDILLVNH	235
Db	181	WQTRRRTPRPGEQVPPVPSQDILLVNH	209

RESULT 11
US-09-109-100-17
; Sequence 17 Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Giaddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260, 0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02

```

: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO: 17
: LENGTH: 209
: TYPE: PRT
: ORGANISM: Homo sapiens
: OS-09-109-100-17

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	Only Match	99.48%	Score 110:	DB4:	Length 209;
	Best Local Similarity	99.5%	Pred. No.	3e-104:	
	Matches 208;	Conservative	1:	Mismatches 0;	Indels 0; Gaps 0;
Qy	27	TOGCSFPHSITSSDFAVKITRELSVDYLDODYPVTVA	SNLODEELCGGIMRYLVAORRMERL	86	
Db	1	TGDCSPHSITSSDFAVKITRELSVDYLDODYPVTVA	SNLODEELCGGIMRYLVAORRMERL	60	
Qy	87	KYVAGSGMGLERVWTEHETVTKAEPQPPSCLEFVYTN	ISRLQETSSQVLAKPMIT	146	
Db	61	KYVAGSGMGLERVWTEHETVTKAEPQPPSCLEFVYTN	ISRLQETSSQVLAKPMIT	120	
Qy	147	RQNFRCLELQCPDSSSLTPPWSPPRELEATAPTAOP	PLLTLTLFVGLLLAAACWCH	206	
Db	121	RNFRCLELQCPDSSSLTPPWSPPRELEATAPTAOP	PLLTLTLFVGLLLAAACWCH	180	
Qy	207	WQTRRRTPRPGQVPPVPSPODLLLVEH	235		
Db	181	WQTRRRTPRPGQVPPVPSPODLLLVEH	209		

```

RESULT 12
US-09-109-100-11
Sequence 11, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: Gradidis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-1 MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-11

```

Query Match	89.2%;	Score 1108;	DB 4;	Length 209;
Best Local Similarity	99.5%;	Pred. No. 4.8e-104;		
Matches 208; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0

QY	27	TQDCSPQHSISSDPVAKRKRELSYUQADYRVYASLUQDELCGMRVLVAQRMERL	86
Db	1	TQDCSPQHSISSDPVAKRKRELSYUQADYRVYASLUQDELCGMRVLVAQRMERL	60
QY	87	KTVAGSMQGLERVATELHEFYTKACAPPEPSCILFQTNISLQETSEQVALKPIIT	146
Db	61	KTVAGSMQGLERVATELHEFYTKACAPPEPSCILFQTNISLQETSEQVALKPIIT	120
QY	147	RQNSRCLQLQCPDSSLLPWPMSRPLEATAPPAOPPLLLLLLPVGLLLAAACGLH	206
Db	121	RQNSRCLQLQCPDSSLLPWPMSRPLEATAPPAOPPLLLLLLPVGLLLAAACGLH	180
QY	207	WQTRRTTRPRGEQVPPVPSQDILLVEH	235
Db	181	WQTRRTTRPRGEQVPPVPSQDILLVEH	209

RESULT 13
US-09-109-100-15
; Sequence 15, Application US/091091000
; patent No. 6291661

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; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-15
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Query Match
Best Local Similarity 89.2%; Score 1108; DB 4; Length 209;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 27 TQDCSFQHSPISSDFAVKIRELSDYLDYPTVANSNLODEELCGGLRWLYLAORWMERL 86
DB 1 TQDCSFQHSPISSDFAVKIRELSDYLDYPTVANSNLODEELCGGLRWLYLAORWMERL 60
QY 87 KTVAGSKMOGLERVTETHEIFVTKCAFQPPSCLEFVQTNISRLLOETSEQLVALKFWIT 146
DB 61 KTVAGSKMOGLERVTETHEIFVTKCAFQPPSCLEFVQTNISRLLOETSEQLVALKFWIT 120
QY 147 RQNFSCLELQCCPDSSSTLPWPSPRPLEATAPTAPOPPLLLLLLPGVGLLLAAACLH 206
DB 121 RQNFSCLELQCCPDSSSTLPWPSPRPLEATAPTAPOPPLLLLLLPGVGLLLAAACLH 180
QY 207 WQTRRRTPRPGEQVPPVPSPODLLVEH 235
DB 181 WQTRRRTPRPGEQVPPVPSPODLLVEH 209
```

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RESULT 14
US-09-109-100-13
; Sequence 13, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-13
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Query Match
Best Local Similarity 89.1%; Score 1107; DB 4; Length 209;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 27 TQDCSFQHSPISSDFAVKIRELSDYLDYPTVANSNLODEELCGGLRWLYLAORWMERL 86
DB 1 TQDCSFQHSPISSDFAVKIRELSDYLDYPTVANSNLODEELCGGLRWLYLAORWMERL 60
QY 87 KTVAGSKMOGLERVTETHEIFVTKCAFQPPSCLEFVQTNISRLLOETSEQLVALKFWIT 146
DB 61 KTVAGSKMOGLERVTETHEIFVTKCAFQPPSCLEFVQTNISRLLOETSEQLVALKFWIT 120
QY 147 RQNFSCLELQCCPDSSSTLPWPSPRPLEATAPTAPOPPLLLLLLPGVGLLLAAACLH 206
DB 121 RQNFSCLELQCCPDSSSTLPWPSPRPLEATAPTAPOPPLLLLLLPGVGLLLAAACLH 180
QY 207 WQTRRRTPRPGEQVPPVPSPODLLVEH 235
DB 181 WQTRRRTPRPGEQVPPVPSPODLLVEH 209
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DB 181 WQTRRRTPRPGEQVPPVPSPODLLVEH 209
RESULT 15
US-09-109-100-8
; Sequence 8, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-8
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Query Match
Best Local Similarity 89.0%; Score 1106; DB 4; Length 209;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 27 TQDCSFQHSPISSDFAVKIRELSDYLDYPTVANSNLODEELCGGLRWLYLAORWMERL 86
DB 1 TQDCSFQHSPISSDFAVKIRELSDYLDYPTVANSNLODEELCGGLRWLYLAORWMERL 60
QY 87 KTVAGSKMOGLERVTETHEIFVTKCAFQPPSCLEFVQTNISRLLOETSEQLVALKFWIT 146
DB 61 KTVAGSKMOGLERVTETHEIFVTKCAFQPPSCLEFVQTNISRLLOETSEQLVALKFWIT 120
QY 147 RQNFSCLELQCCPDSSSTLPWPSPRPLEATAPTAPOPPLLLLLLPGVGLLLAAACLH 206
DB 121 RQNFSCLELQCCPDSSSTLPWPSPRPLEATAPTAPOPPLLLLLLPGVGLLLAAACLH 180
QY 207 WQTRRRTPRPGEQVPPVPSPODLLVEH 235
DB 181 WQTRRRTPRPGEQVPPVPSPODLLVEH 209
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Search completed: November 24, 2002, 10:12:44
Job time : 15.1116 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 24, 2002, 10:08:46 ; Search time 14.3755 Seconds
(without alignments)
1544.781 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223

Sequence: 1 MTVLAPAMSPNSLLILLLL.....MQRARRGELHPGVLPSPHP 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1223	100.0	231	2	A49265	flt3/flk-2 ligand
2	879	71.9	220	2	S43291	FLT3/FLK2 ligand (
3	879	71.9	220	2	I58343	flt3 ligand isoform
4	768.5	62.8	235	2	I38440	FLT3 ligand - huma
5	616.5	50.4	245	2	S43293	FLT3/FLK2 ligand (
6	594.5	48.6	178	2	I39076	FLT3 ligand alterna
7	95.5	7.8	909	1	A54809	disease resistance
8	88	7.2	843	2	T01438	hypothetical prote
9	87	7.1	291	2	AF0123	probable antigenic
10	86	7.0	962	2	C71617	SERA antigen/papal
11	85	6.9	181	2	T20323	hypothetical prote
12	84.5	6.9	939	2	E82121	peptidase, insulin
13	84	6.9	1409	2	T37188	presynaptic activi
14	83.5	6.8	552	1	A31401	macrophage colony-
15	83.5	6.8	552	1	S35703	colony-stimulating
16	83.5	6.8	2476	2	T34022	zonadhesin - pig
17	82.5	6.7	378	2	S00842	leukostallin precu
18	82.5	6.7	431	2	T04868	hypothetical prote
19	81	6.6	4131	2	T21085	hypothetical prote
20	80.5	6.6	391	2	B40892	apolipoprotein A-I
21	80.5	6.6	394	2	A25281	apolipoprotein A-I
22	80.5	6.6	395	2	A40892	apolipoprotein A-I
23	80	6.5	382	2	E84527	hypothetical prote
24	79.5	6.5	399	2	C40892	apolipoprotein A-I
25	79.5	6.5	745	2	T38299	probable beta-adap
26	79	6.5	1101	2	S38108	hypothetical prote
27	78.5	6.4	315	2	T24821	hypothetical prote
28	78.5	6.4	315	2	T24821	hypothetical prote
29	78.5	6.4	379	2	T11349	ubiquinol-cytochro

30	78.5	6.4	468	2	T23091	hypothetical prote
31	78.5	6.4	3068	1	A44062	genome polyprotein
32	78	6.4	224	2	I37243	CMF-35 antigen -
33	78	6.4	743	2	T34632	probable bi-functi
34	78	6.4	806	2	E64221	phenylalanine-tRNA
35	78	6.4	908	2	S51293	probable membrane
36	78	6.4	1601	2	AE2011	hypothetical prote
37	78	6.4	1715	2	T06145	disease resistance
38	77.5	6.3	266	2	A45844	MHC class II histo
39	77.5	6.3	456	2	B72130	frame-shift with c
40	77.5	6.3	579	2	JC7629	membrane-type friz
41	77.5	6.3	746	2	S67203	probable membrane
42	77.5	6.3	774	2	B86492	hypothetical prote
43	77.5	6.3	774	2	B81540	hypothetical prote
44	77.5	6.3	811	2	E72003	hypothetical prote
45	77	6.3	619	2	D86509	S/T protein kinase

ALIGNMENTS

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RESULT 1
A49265
flt3/flk-2 ligand precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #Sequence-Revision 13-Jan-1995 #text-change 08-Oct-1999
C:Accession: A49265; I49347; I49346; S43290
R:Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Holl
D.; Williams, D.E.; Beckmann, M.P.
Cell 75, 1157-1167, 1993
A:Title: Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor: a
A:Reference number: A49265; MUID:94084791; PMID:7505204
A:Accession: A49265
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-231 <LYM>
A:Cross-references: GB:I23636; NID:g439441; PIDN:AAA39436.1; PID:g439442
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.
Oncogene 11, 1165-1172, 1995
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: I39075; MUID:96032581; PMID:7566977
A:Accession: I49347
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-163, 'G', 165, 'HYAG' <RES>
A:Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90952.1; PID:g1072041
A:Accession: I49346
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-197, 'L', 198-231 <RE2>
A:Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040
R:Hannun, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.;
felt, A.; Muench, M.; Kelnier, G.; Nankkawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik
Nature 368, 643-648, 1994
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopo
A:Reference number: S43290; MUID:94195428; PMID:8145851
A:Accession: S43290
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-197, 'L', 198-231 <HAN>
A:Experimental source: clone T110
A:Note: the sequence from Fig. 2c is inconsistent with that from Fig. 2a in having 4-
C:Genetics:
A:introns: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3
C:Keywords: transmembrane protein
Query Match 100.0%; Score 1223; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.9e-101;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 VAVNLODEKCKALMSFLAORMIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120
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 Db 61 VAVNLODEKCKALMSFLAORMIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120
 QY 121 LRFVOTNISHLKDTCTQLLALKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPILEAT 180
 |||||
 Db 121 LRFVOTNISHLKDTCTQLLALKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPILEAT 180
 QY 181 ELPEPRRQOLLILLPLTVLLAAAGLWQRRARRRGLHGVPLPSHP 231
 |||||
 Db 181 ELPEPRRQOLLILLPLTVLLAAAGLWQRRARRRGLHGVPLPSHP 231

RESULT 2
 S43291
 FLT3/FLK2 ligand (clone T118) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
 C:Accession: S43291
 R:Hanum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Ka
 felt, A.; Muench, M.; Kellner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A
 Nature 368, 643-648, 1994
 A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic
 A:Reference number: S43290; MUID:94195428; PMID:8145851
 A:Accession: S43291
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-220 <HAN>

Query Match 71.9%; Score 879; DB 2; Length 220;
 Best Local Similarity 82.3%; Pred. No. 1e-70;
 Matches 177; Conservative 5; Mismatches 21; Indels 12; Gaps 3;

QY 1 MTVALPAMSPNSLSLLLSLSPCLRGTPDCYFSHSPISSENFVKFRELDHLKDYPT 60
 |||||
 Db 1 MTVALPAMSPNSLSLLLSLSPCLRGTPDCYFSHSPISSENFVKFRELDHLKDYPT 60

QY 61 VAVNLODEKCKALMSFLAORMIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120
 |||||
 Db 61 VAVNLODEKCKALMSFLAORMIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120

QY 121 LRFVOTNISHLKDTCTQLLALKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPILEAT 180
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 Db 121 LRFVOTNISHLKDTCTQLLALKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPILEAT 180

QY 177 LEATELPEPRRQOLLILLPLTVLLAAAGLWQRRARRRGLHGVPLPSHP 231
 |||||
 Db 177 LEATELPEPRRQOLLILLPLTVLLAAAGLWQRRARRRGLHGVPLPSHP 231

RESULT 3
 S58343
 FLT3 ligand isoform 5H - mouse
 C:Species: Mus sp. (mouse)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
 C:Accession: S58343
 R:Lyman, S.D.; James, L.; Escobar, S.; Downey, H.; de Vries, P.; Brasel, K.; Stocking, K
 Oncogene 10, 149-157, 1995
 A:Title: Identification of soluble and membrane-bound isoforms of the murine flt3 ligand
 A:Reference number: S58343; MUID:95124710; PMID:7824267
 A:Accession: S58343
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-220 <RES>
 A:Cross-references: GB:S76459; MUID:9913479; PIDN:AA833069.1; PID:9913480

Query Match 71.9%; Score 879; DB 2; Length 220;
 Best Local Similarity 82.3%; Pred. No. 1e-70;
 Matches 177; Conservative 5; Mismatches 21; Indels 12; Gaps 3;

QY 1 MTVALPAMSPNSLSLLLSLSPCLRGTPDCYFSHSPISSENFVKFRELDHLKDYPT 60
 |||||

Db 1 MTVALPAMSPNSLSLLLSLSPCLRGTPDCYFSHSPISSENFVKFRELDHLKDYPT 60
 |||||
 QY 61 VAVNLODEKCKALMSFLAORMIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120
 |||||
 Db 61 VAVNLODEKCKALMSFLAORMIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120

QY 121 LRFVOTNISHLKDTCTQLLALKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPILEAT 180
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 Db 121 LRFVOTNISHLKDTCTQLLALKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPILEAT 180

QY 177 LEATELPEPRRQOLLILLPLTVLLAAAGLWQRRARRRGLHGVPLPSHP 231
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 Db 177 LEATELPEPRRQOLLILLPLTVLLAAAGLWQRRARRRGLHGVPLPSHP 231

RESULT 4
 I38440
 flt3 ligand - human
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
 C:Accession: I38440; I39075; S43292
 R:Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S.S.; Downe
 Blood 83, 2795-2801, 1994
 A:Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor fo
 A:Reference number: I38440; MUID:94235842; PMID:8180375
 A:Accession: I38440
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-235 <RES>
 A:Cross-references: EMBL:U028874; MUID:9494978; PIDN:AAA19825.1; PID:9494979
 R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.
 Oncogene 11, 1165-1172, 1995
 A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
 A:Reference number: I39075; MUID:96032581; PMID:7566977
 A:Accession: I39075
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-235 <RES>
 A:Cross-references: EMBL:U028874; MUID:9494978; PIDN:AAA19825.1; PID:9494979
 R:Hanum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.;
 felt, A.; Muench, M.; Kellner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik
 Nature 368, 643-648, 1994
 A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic
 A:Reference number: S43290; MUID:94195428; PMID:8145851
 A:Accession: S43292
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-71, 'A', 73-235 <HAN>
 A:Cross-references: GB:U04806; MUID:9483844; PIDN:AAA17999.1; PID:9483845
 A>Note: the authors translated the codon AGT for residue 25 as Met
 C:Genetics: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3

Query Match 62.8%; Score 768.5; DB 2; Length 235;
 Best Local Similarity 70.3%; Pred. No. 7.1e-61;
 Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MTVALPAMSPNSLSLLLSLSPCLRGTPDCYFSHSPISSENFVKFRELDHLKDYPT 60
 |||||
 Db 1 MTVALPAMSPNSLSLLLSLSPCLRGTPDCYFSHSPISSENFVKFRELDHLKDYPT 60

QY 61 VAVNLODEKCKALMSFLAORMIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120
 |||||
 Db 61 VAVNLODEKCKALMSFLAORMIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120

QY 121 LRFVOTNISHLKDTCTQLLALKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPILEAT 180
 |||||
 Db 121 LRFVOTNISHLKDTCTQLLALKPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPILEAT 180

QY 177 LEATELPEPRRQOLLILLPLTVLLAAAGLWQRRARRRGLHGVPLPSHP 231
 |||||
 Db 177 LEATELPEPRRQOLLILLPLTVLLAAAGLWQRRARRRGLHGVPLPSHP 231

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RESULT 5
 S43293
 FLT3/FLT2 ligand (clone S109) - human
 C:Species: Homo sapiens (man)
 C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
 C:Accession: S43293
 R:Hannun, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kiehl, A.; Wuensch, M.; Kellner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A.
 Nature 368, 643-648, 1994
 A:Title: Ligand for FLT3/FLT2 receptor tyrosine kinase regulates growth of haematopoietic cells
 A:Reference number: S43290; MUID:94195428; PMID:8145851
 A:Accession: S43293
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-245 <HMAN>
 A:Note: the authors translated the codon AGT for residue 25 as Met

Query Match	50.48;	Score 616.5;	DB 2;	Length 245;
Best Local Similarity	57.08;	Pred. No. 2.4e-47;		
Matches 139;	Conservative 16;	Mismatches 54;	Indels 35;	Gaps 6;

QY 1 MTVLAPAMSPNNLLLSLSCLRGTPDCYRSHSPSSNFEYKFRRETDHLKDDPYVT 60
|||||:::|||||
Db 1 MTVLAPAMSP-ITVLLLSLLSSGLMGTDCCSHSPSSSDFAVKIRELSDYLLQDDPYVT 59

QY 61 VAVNLDDEKCKALMSLFLAQRMIEQLKVAGSKMÖTLEDVNTIEHFVTSCTFÖEIP_{ECC} 120
|| ||||| : ||| : ||||| ||| ||||| ||| ||| |
Db 60 VASNLDDDELGCALRWLVLAQRMERIKTVAGSKMÖGLTERVNTEIHFVKCAFGPPSPC 119

QY 121 LRFVQTINISHLKDFCTQGLALPKFCIGKACQNRSRCLEVCQCQPSSSTLTPRRSPIALTEAT 180
| | | | | : : : | | : | | : | | : | | :
DB 120 LRFVQTINISRLLOETSEQLVALKPWITR--QNFSRCLELCQCQPGAPRPQSP-GPAACGAL 176

```

QY      101 ELRPKRP-----KQLLLLLLPLVLAAAGLRQRRRRGELHGVPL 227
          | | | | | | | | | | | | | | | | | | | | | |
Db      177 TWRPRHGEDTEAHNRGSPANGCI-----AW---TQRLARGSLPWAPL 218

```

Qy	228	PSHP	231
Db	219	IPSP	222

RESULT 6
I39076

C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: I35076

A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: 139075; MUID:96032581; PMID:7566977
Oncogene 11, 1165-1172, 1995

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-178 <RES>

C, Genetics: A; Introns: 11/3; 48/3; 66/3; 114/3; 161/1

Best Local Similarity 73.6%; Pred. No. 1.5e-45;
Matches 120; Conservative 14; Mismatches 26; Indels 3; Gaps 2;

```

0v      61 VAVNLODEKHCKALWSTLETAORWTFEOI KTVACSKMOTI I EDVAMETHEVMSCEEOOI DEG
Db      1 MTVLAPAWSP -TYYLLLLLLSGISGTQDCSFQHSPPSSDFAVKIRELSYLLQDPVPT
          :: ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Db 60 VASNIODEELCGLMRLVLAQRMERLKTVASGSKMÖGLIERVNTFIIHFVTKCAFQPPSC 119

```
QY 121 LRFVQNTISHLKDTCTYLLAKPCIGKACQNFSSRCLEVVQCP 163
      |||||::: ||:|||| : |||||:||||
Db 120 LRFVQNTISRLLOETSSQVLAIKPWTR--QNSRSCLELQCCP 160
```

RESULT 7
A54809

N:Alternate names: protein F20B18.200
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000

R.Mindrinos, M.:Katagiri, F.; Yu, G.L.; Ausubel, F.M.
Cell 78, 1089-1099, 1994
Article: The Arabidopsis thaliana disease resistance gene RPS2 encodes a protein containing a leucine-rich repeat domain

A/Accession: A54809
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A.Positions: 1-909 (MT)

Artibeus pesq. of arachnoidosis thalassa: a leucocytic repeat class of β -act distal

A;Reference number: A54811; MUID:94377978; PMID:8091210
A;Accession: A54811
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA; mRNA

AACross-references: GB:U14158; NID:5548085; PIDN:AAA21874.1; PID:5548086
B:Bevan, M.; Rose, M.; Hempel, S.; Ethlian, K.D.; Hohense, J.; Mewes, H.W.; Mayer, K.
submitted to the Protein Sequence Database, March 1999

A:Reference Number: 413203
A:Accession: T04264
A:Molecule type: DNA
A:Residues: 1-909 <BEV>

A:Experimental source: cultivar Columbia; BAC clone F20B18
 C:Genetics:
 A:Gene: RPS2

A:Note: P20B18, 200
C:Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein rep
C:Keywords: leucine zipper; membrane protein; nucleotide binding

Query Match	7.8%;	Score 95.5;	DB 1;	Length 909;
Best Local Similarity	22.8%;	Pred. No. 2.1;		
Matches	55;	Conservative	40;	Mismatches 89; Indels 57; Gaps 11.

[illegible]

```

QY      63  -----VNLDKHCALMSLEL-----AQRWTEQLKTV-----AGSKMOTLLEDVNT 104
          ||: ||      : ||      | : : :      || : : : ||
Db      595  VLPQELGNERLKHLDQRTQFQTIPDAICWLSKEVLNLYYSAWGELSGEDEAE 654

```

```

QY 105 EIH-----VTSCHFQPLPECLRF--QQTNISLLKDKTQLLAIK-PCIGK 146
      1: 1      1: 1: 1      1: 1: 1: 1: 1: 1: 1: 1: 1: 1:
Db 655 ELGRADLEYENLTTLGITVLSLETLLKTLFEFGALHKHQHLHVEECNELLYFNLPSTLN 714

```

```
QY      149 ACQNNSRCLEVCQCQPDSSTLPEPRSPIDALETELRPEPRRQLLLLLLLPLTVLLAAW 208
          :| | |::| | |::|| | | |
Db      715 HGRNLR-LSIKSCHDELYV---TPADFENDWLPS--LEVLTSLHNTTRV-----W 762
```

QY	209	G	209
Db	763	G	763

RESULT 8
T01438
hypothetical protein GS034D21.1 - human (fragment)

```

0Y 109 VMSCFOPDPE---C--LRFVQTNISHL-----LKDTCTQLLAIKPCIGKACON 152
  ::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 75 TSTDTSTDPDPLBQCNPI NTNNNT PET DPMU DDMU ONT KASNOU DPM DMMU DACTS 134

```

	conservative	mismatches	indels	gaps
13 SLLILLIISPCURGTPDCYFESHSPISNFEKVKFREITDHLIKD-----YPTVAANVNIOD 67	39;	24;	59;	44;
Matches	39;	conservative	24;	mismatches
Matches	39;	conservative	24;	mismatches

Query Match	7.0%;	Score 85;	DB 2;	Length 181;
Best Local Similarity	23.5%;	Pred. No. 2.8;		
Matches	30;	Concentrations	74;	Mismatches 50;
				Indels 44;
				Gaps 10;

13 SLILLILLSPCLRGTPDCYFESHSPRISSNFKVKFKRELTDHLKD-----YPVTVAVNLOD 67

```

Db      8 TILPLFLISKAENSPIDCSKDDLTQITVTCRPLAKLIDEMKKKNPNLNGSPSVETLN  KM  66
Qy      68 EKHCAALMSLPLAOWIWIQDLKTAVAGSKMOTLLEDVYNTLHVTSC---TFQPLP-----  118
Db      67 SGYCK-----FAMSCVSPAKCPATEKMS---KEATMKTIDYFSGPAOCCA  111
Qy      119 -----ECLEFVQTNISHLKD-TCTOLLARPCI-----GNAC  150
Db      112 KIKASNDKTECVQWTFSDKSRNSTDOKCAQFKAKKQCIEMQFGKAC  157

```

RESULT 12
E82121
peptidase, insulinase family VC2072 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
C:Species: *Vibrio cholerae*
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: E82121
R:Heidelberg, D.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
Charidson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.
1. R.R.; Melnikos, J.J.; Venter, J.C.; Fraser, C.M.
N:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
N:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: E82121
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-939 <HE>
A:Cross-references: GB:AE004281; GB:AE003852; NID:99656616; PIDN:AN95218.1; GSPB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2072
A:Map position: 1
C:Superfamily: InsuLysin

Query Match	6.9%	Score 845;	DB 2;	Length 939;
Best Local Similarity	24.6%	Pred. No. 20;		
Matches	61;	Conservative	30;	Mismatches 72; Indels 85; Gaps 15;
QY	40	SNFKVKEPRLTDHLKDY-----PVTAV-----	NLDEKHKALMSLFLAQRWTEQ	86
		: : : : : : : : :		
Db	587	SGFSQKLTQMLEVILIRKFAQRDFQPKRFATIKQMTTRMNRNAAHDKPISTOLFNAATGGLIQ		646
QY	87	LKTAVGSKMOTLLEDVUNE--IHFTSCTFO-----	PLPECIRFVQNTSHLK	133
		: : : : :		
Db	647	PNNPPRAIELLAIDVOYBELAHNFYDTILLSQLHVEFMFYGDMPAAEAK-----	MAEVLK	701
QY	134	DTC-----TQIALKPCG--GKACNFSRCLEVOCCDPSSSTL-----	LPSPSFIAL--	177
		: : : : : : :		
Db	702	DALRVGGQTYESLSPRLVWLGRS--GTFQR--EYCCQODSDSAIVVYVYQSHVEVPSR--	IbLY	757
QY	178	-----EATLEPBRPRROLILLL--LPLTLVLLAAMGLIRQARRRGELTIPGYPL		227
		: : : : : : :		
Db	758	SLANHLMSATTFEHEIRTRTQQLGYVVGTCGNMPL-----	NNRIFGLIL	797
QY	228	-----PSHP	231	
Db	798	IYQSPSAP	805	

RESULT 13
T37188
presynaptic activity regulator aex-3 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000
C.Accession: T37188
R.Leimbac, D., Minx, M.
submitted to the EMBL Data Library, February 1996
A.Description: The sequence of C. elegans cosmid C02H7.
A.Reference number: Z20523
A.Accession: T37188
A.Status: translated from GB/EMBL/DDBJ
A.Molecule type: DNA

```

A:Residues: 1-1409 <EMI>
A:Cross-references: LBL:U04945; PIDN:AA047926.1; GSPDB:GND00029
A:Experimental source: strain Bristol N2; clone C02H7
C:Genetics:
A:Gene: aex-3; CESP:C02H7.3
A:Map position: X
A:Introns: 77/1; 136/2; 183/2; 232/3; 283/3; 386/3; 427/3; 527/3; 577/1; 699/3; 782/2

Query Match      6 9%  Score 84;  DB 2;  Length 1409;
Best Local Similarity 23 9%  Pred. NO. 36;
Matches 54;  Conservative 31;  Mismatches 73;  Indels 68;  Gaps 13;

```

```

QY 4 IAPASPSNLLILLLLISPCLAGTPOCYFSHSPISNFKYXREL-TDHLIKDQPVVA 62
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 317 ILPAVPAEAE--QLLLAPPEFLIGPSSFFHNR-----KIRLEPDIIVLVID-D-TNC 365

QY 63 VNIODEKHCALMSLEL-----AQRMEQLKTAVAGSMOTLLEDVATE----- 105
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 366 LQVPDD-----LYIPDLPEPDATHLKERLKN-AINKMTTMYDNETSVYDADFGIDI 416

QY 106 -----IHEVTS-----TROPLECRIFVQTNISHLIKDTQYLLAK 143
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 417 DSDVACRYAMQFENSNANVEGNFSEHRTLTLXLYPRVVSLOTDSFLRSRQOCYOLIT-D 475

QY 144 PCIGKACNFSKCLEVOCO-PDSSFLPLPRSPILAEATELEPPRR 188
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 476 LCRTOAVEYFAEC-----CLCEKNETFV--RVOAGTESSEYQGDARK 515

```

RESULT 14

A11401

macrophage colony-stimulating factor precursor - mouse

N.Alternate names: colony-stimulating factor 1; M-CSF

C.Species: Mus musculus (house mouse)

C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C.Accession: A11401; JN0294; A25575; A23166; A28883

R.Planner: M.B.; Martill, G.A.; Noble, J.A.; Wiltman, V.P.; Warren, M.K.; McGrogan, M.;

Proc. Natl. Acad. Sci. U.S.A. 85, 6706-6710, 1988

A.Title: cDNA cloning and expression of murine macrophage colony-stimulating factor f

A.Reference number: A11401; MUID:88320507; PMID:2457916

A.Accession: A31401

A.Molecule type: mRNA

A.Residues: 1-552 <IAD>

A.Cross-references: GB:M1952; GB:J03862; NID:g192804; PIDN:AA37481.1; PID:g309199

R.Harrington, M.A.; Benberg, H.J.; Saxman, S.; Pedigo, L.M.; Dab, R.; Brommeyer, H.

Gene 102, 165-170, 1991

A>Title: Cloning and characterization of the murine promoter for the colony-stimulat

A.Reference number: JN0294; MUID:91340149; PMID:1874443

A.Accession: JN0294

A.Molecule type: DNA

A.Residues: 1-13 <HAR>

A.Cross-references: GB:M81316; GB:M61708; NID:g192802; PIDN:AA19866.1; PID:g192803

R.Delamater, J.F.; Hession, C.; Semon, D.; Gough, N.M.; Rothenbuhler, R.; Metmod, J.

Nucleic Acids Res. 15, 2389-2390, 1987

A>Title: Nucleotide sequence of a cDNA encoding murine CSF-1 (macrophage-CSF).

A.Reference number: A26575; MUID:87174763; PMID:3494232

A.Accession: A26575

A.Molecule type: mRNA

A.Residues: 1-5, 'R', 7-245, 'A', 247-552

R.Ben-Avram, C.M.; Shively, J.E.; Shaduck, R.K.; Waheed, A.; Rajavashisth, T.; Lusis

Proc. Natl. Acad. Sci. U.S.A. 82, 4486-4489, 1985

A.Reference number: A23166; MUID:85242709; PMID:3925458

A.Accession: A23166

A.Molecule type: protein

A.Residues: 33-39, 'CC', 42-57 <BEN>

R.Rajavashisth, T.B.; Eng, R.; Shaduck, R.K.; Mahed, A.; Ben-Avram, C.M.; Shively,

Proc. Natl. Acad. Sci. U.S.A. 84, 1157-1161, 1987

A>Title: Cloning and tissue-specific expression of mouse macrophage colony-stimulat

A.Reference number: A25883; MUID:87147232; PMID:3493488

A.Accession: A25883

A.Molecule type: mRNA

A.Residues: 1-2, 4-5, 'NPR', 9-100 <RAJ>

A.Cross-references: GB:M15692; NID:g192800; PIDN:AA37480.1; PID:g192801

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 24, 2002, 10:03:41 ; Search time 8.42704 Seconds

(without alignments)
1136.939 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223
Sequence: 1 MTVLAFWSPNSLLLLLLL.....MQRARRRGLHPGVLPSPHP 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1212.5	99.1	232	1	FLJL_MOUSE
2	768.5	62.8	235	1	FLJL_HUMAN
3	89.5	7.3	941	1	GBR2_HUMAN
4	89	7.3	815	1	AD15_MOUSE
5	87	7.1	816	1	AD15_RAT
6	84.5	6.9	1205	1	AT53_HUMAN
7	84	6.9	1409	1	AEX3_CAEEL
8	83.5	6.8	352	1	CSF1_MOUSE
9	83.5	6.8	2476	1	ZAN_PIG
10	82.5	6.7	378	1	LEUR_RAT
11	80.5	6.6	395	1	AP44_MOUSE
12	80	6.5	195	1	INT_OVIMO
13	79	6.5	1101	1	YAG2_SCHPO
14	78.5	6.4	122	1	Y722_MCTU
15	78.5	6.4	1208	1	RCO4_HUMAN
16	78.5	6.4	3068	1	POLG_PEMVC
17	78	6.4	224	1	CM35_HUMAN
18	78	6.4	806	1	SYFB_MYCGE
19	78	6.4	908	1	Y611_YEAST
20	77.5	6.3	266	1	HB2D_CAFNA
21	77.5	6.3	940	1	GBR2_RAT
22	76.5	6.3	222	1	YB95_MERTH
23	76.5	6.3	326	1	VS09_ROTSH
24	76.5	6.3	1296	1	ASAL_ENMFA
25	76.5	6.3	3660	1	DMD_CHICK
26	76	6.2	438	1	PR11_DROME
27	76	6.2	977	1	EP42_MOUSE
28	75.5	6.2	379	1	CYB_CAMDR
29	75.5	6.2	577	1	TRBM_MOUSE
30	75.5	6.2	4543	1	LRP1_CHICK
31	75	6.1	433	1	ENOA_SCEUN
32	75	6.1	513	1	AVR2_HUMAN
33	75	6.1	732	1	KELL_HUMAN

34	75	6.1	758	1	VKGC_HUMAN	P38435 homo sapien
35	75	6.1	887	1	SM6B_RAT	P07041 rattus norv
36	74.5	6.1	326	1	VS09_ROT5	P08406 porcine rot
37	74.5	6.1	356	1	TRBM_BOVIN	P06579 bos taurus
38	74	6.1	326	1	VS09_ROTNR	P1855 human rotav
39	74	6.1	326	1	VS09_ROTNR	P12476 rhesus rota
40	74	6.1	448	1	BCN1_MOUSE	P08597 mus musculu
41	74	6.1	450	1	BCN1_HUMAN	Q14457 homo sapien
42	74	6.1	478	1	BM3B_HUMAN	P5107 homo sapien
43	74	6.1	513	1	AVR2_BOVIN	Q28043 bos taurus
44	74	6.1	513	1	AVR2_MOUSE	P27038 mus musculu
45	74	6.1	618	1	DLT3_HUMAN	Q9nj17 homo sapien

ALIGNMENTS

RESULT 1
FLJL_MOUSE STANDARD; PRT; 232 AA.
AC P49772: Q64085;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3 ligand) (Flt3L).
GN FLT3LG OR FLT3L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94195428; PubMed=8145851;
RA Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S., Bazan J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J., Muench M., Keiser G., Namikawa R., Rennick D., Roncarolo M.G., Zlotnik A., Rosnet O., Dubreuil P., Birbaumer D., Lee F.;
RA "Ligand for FLT3/ELK receptor tyrosine kinase regulates growth of haematopoietic stem cells and is encoded by variant RNAs.";
RT Nature 368:643-648(1994).
RL
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=STL/J;
RC MEDLINE=94084791; PubMed=7505204;
RA Lyman S.D., James L., Vandenbos T., Devries P., Brasel K., Gliniak B., Hollingsworth L.T., Picha K.S., McKenna H.J., Foxworth D., Williams D.E., Beckmann M.P.;
RA "Molecular cloning of a ligand for the flt3/Flk-2 tyrosine kinase receptor: a proliferative factor for primitive hematopoietic cells.";
RT Cell 75:1157-1167(1993).
RL
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=96032581; PubMed=7566977;
RA Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L., Escobar S.;
RA "Structural analysis of human and murine flt3 ligand genomic loci.";
RT Oncogene 11:1165-1172(1995).
RL
RN [4]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=95124710; PubMed=78424267;
RA Lyman S.D., James L., Escobar S., Downey H., de Vries P., Brasel K., Stocking K., Beckmann M.P., Copeland N.G., Cleveland L.S.;
RA "Identification of soluble and membrane-bound isoforms of the murine flt3 ligand generated by alternative splicing of mRNAs.";
RT Oncogene 10:149-157(1995).
RL
RN [5]
RP SEQUENCE FROM N.A.
RX McClanahan T., Culpepper J., Campbell D., Wagner J., Mattson J., Franz-Bacon K., Mattson J., Tsai S., Luh J., Guilmer M.J.,

Db 181 ELPEPRPQLTLTLLLTPLTVLAAAWGRLRMORARRRGELHPGVLPSPH 232

|||||

RESULT 2
FL3L_HUMAN STANDARD; PRT; 235 AA.

ID FL3L_HUMAN
AC P49771;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (flt3 ligand) (flt3l).
DE FLI3LG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE FROM N.A.
RA Hamann C., Culpepper J., Campbell D., McClanahan T., Zurawski S., Bazan J.F., Kastlein R., Hudak S., Wagner J., Mattson J., Luh J., Duda G., Marina N., Peterson D., Menon S., Shanfield A., Muench M., Kolner G., Namikawa R., Rennick D., Roncarolo M.G., Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.;
RT "Ligand for FLT3/FLT3L receptor tyrosine kinase regulates growth of hematopoietic stem cells and is encoded by variant RNAs.";
RL Nature 368:643-648(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94195428; PubMed=8145851;
RA Hamann C., Culpepper J., Campbell D., McClanahan T., Zurawski S., Bazan J.F., Kastlein R., Hudak S., Wagner J., Mattson J., Luh J., Duda G., Marina N., Peterson D., Menon S., Shanfield A., Muench M., Kolner G., Namikawa R., Rennick D., Roncarolo M.G., Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.;
RT "Cloning of the human homologue of the murine flt3 ligand: a growth factor for early hematopoietic progenitor cells.";
RL Blood 83:2795-2801(1994).
RN [3]
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RX MEDLINE=96032581; PubMed=7566977;
RA Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L., Escobar S.;
RT "Structural analysis of human and murine flt3 ligand genomic loci.";
RL Oncogene 11:1165-1172(1995).
RN [4]
RX X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA MEDLINE=20343011; PubMed=10681197;
SA Savides S.N., Boone T., Karplus P.A.;
RT "Flt3 ligand structure and unexpected commonalities of helical bundles and cysteine knots.";
RL Nat. Struct. Biol. 7:486-491(2000).
CC -!- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING FACTORS AND INTERLEUKINS.
CC -!- SUBUNIT: Homodimer (isoform 2).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1); secreted (isoform 2).
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; a 1/membrane-bound (shown here) and 2/soluble; are produced by alternative splicing

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EMBL: U04806; AAA17999.1; -
DR EMBL: U03858; AAA19825.1; -
DR EMBL: U29874; AAA09050.1; -
EMBL: U29874; AAA09050.1; -
PDB: 1ETE: 09-JUN-00.

DR Genew; HGNC:3766; FLT3LG.
 DR MIM; 600007; -
 DR InterPro: IPR004213; FLT3_Lig.
 DR Pfam: PF02947; flt3_Lig; 1
 KM Cytochrome; Glycoprotein; Transmembrane; Alternative splicing; Signal;
 KW 3D-structure.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 235 SL CYTOKINE.
 FT DOMAIN 27 184 EXTRACELLULAR (POTENTIAL).
 FT TRAMEM 185 205 POTENTIAL.
 FT DOMAIN 206 235 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 30 111
 FT DISULFID 70 153
 FT DISULFID 119 158
 FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 161 178 DSSLPWPSPRPPLAATA -> VETVHRVSQDGLLTS
 FT VARSPLIC 179 235 (IN ISOFORM 2).
 FT VARSPLIC 72 72 MISSING (IN ISOFORM 2).
 FT CONFLICT 72 72 G -> A (IN REF. 1).
 SQ SEQUENCE 235 AA; 26416 MW; 73B95BF63B4CECF CRC64;
 Query Match 62.8%; Score 768.5; DB 1; Length 235;
 Best Local Similarity 70.3%; Pred. No. 2.4e-60;
 Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;
 QY 1 MVTYLAAPSNSLLILLLISPCLRGPPDYCFSSHPSSNFKVKFRETDHLTKDYPT 60
 DB 1 MVTYLAAPSNSLLILLLISPCLRGPPDYCFSSHPSSNFKVKFRETDHLTKDYPT 59
 QY 61 VAVNLDEHCKALMSFLAQRWIEQLKTAVAGSKMOTLEDNTEIHFVTSCTFQPLEPC 120
 DB 60 VASNLODELCGIMLVLAQRWMEKLTAVAGSKMOTLEDNTEIHFVTSCTFQPLEPC 119
 QY 121 LRFVOTNISHLKDTCTQLALPKLGKACQNFSCLEYOCQDPSSTLLPPSPALAEAT 180
 DB 120 LRFVOTNISHLKDTCTQLALPKLGKACQNFSCLEYOCQDPSSTLLPPSPALAEAT 177
 QY 181 ELRPPRRQLLLPLTLVILAAAGMLRQRRARR---GELHPGVPLP 228
 DB 178 APTAPQPP--LLLLLPVGLLLAAMCLHMQRTRRRPRPEGVPPVPS 227
 RESULT 3
 GBR2_HUMAN STANDARD. PRT: 941 AA.
 AC 073899; 075974; 075975; Q9UN99; Q9UNR1; Q9PLR2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Gamma-aminobutyric acid type B receptor, subunit 2 precursor (GABA-B receptor 2) (GABA-B-R2) (gb2) (GABABR2) (G protein-coupled receptor 51) (GPR 51) (HG20).
 GN GABABR2 OR GPR51.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A. (ISOFORM 2A).
 RC TISSUE=Cerebellum;
 RX MEDLINE=99087321; PubMed=9872316;
 RA White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H., Barnes A.A., Emson P., Ford S.M., Marshall F.H.;
 RT "Heterodimerization is required for the formation of a functional GABA(B) receptor."
 RT Nature 396:679-682(1998).
 RL [2]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2A; 2B AND 2C).
 RC TISSUE=Brain;
 RX MEDLINE=20193514; PubMed=10727622;
 RA Clark J.A., Mezey E., Lam A.S., Bonner T.I.;
 RT "Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";

RL Brain Res. 860:41-52(2000).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2A).
 RA Liu M., Parker R., McCrea K., Watson J., Baker E., Sutherland G., Herzog H.;
 RT "Cloning and characterization of a novel human GABA-B receptor subtype with high affinity for GABA and low affinity for baclofen."
 RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2A).
 RC TISSUE=Hippocampus;
 RA Borowsky B., Laz T., Gerald C.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 2A).
 RC TISSUE=Retal brain;
 RX MEDLINE=99189236; PubMed=10087195;
 RA Ng G.Y.K., McDonald T., Bonner T., Rigby M., Heavens R., Whiting P., Chateauf A., Coulombe N., Kargman S., Caskey T., Evans J.F., O'Neill G.P., Liu Q.;
 RT "Cloning of a novel G-protein-coupled receptor GPR 51 resembling GABAB receptors expressed predominantly in nervous tissues and mapped proximal to the hereditary sensory neuropathy type 1 locus on chromosome 9."
 RT Genomics 56:288-295(1999).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 2A), AND VARIANTS PHE-628 AND ALA-869.
 RC TISSUE=Brain;
 RX MEDLINE=99261199; PubMed=10328880;
 RA Martin S.C., Russek S.J., Farb D.H.;
 RT "Molecular identification of the human GABABR2: cell surface expression and coupling to adenylyl cyclase in the absence of GABABR1."
 RT Mol. Cell. Neurosci. 13:180-191(1999).
 RN [7]
 RP RIA-R2 INTERACTION.
 RX MEDLINE=99175124; PubMed=10075644;
 RA Ng G.Y.K., Clark J., Coulombe N., Ethier N., Sullivan R., Kargman S., Chateauf A., Tsukamoto N., McDonald T., Whiting P., Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F., Bonner T.I., O'Neill G.P.;
 RT "Identification of a GABAB receptor subunit, gb2, required for functional GABAB receptor activity."
 RT J. Biol. Chem. 274:7607-7610(1999).
 RN [8]
 RP RIA-R2 INTERACTION.
 RX MEDLINE=20237752; PubMed=10773016;
 RA Sullivan R., Chateauf A., Coulombe N., Kolakowski L.F. Jr., Johnson M.P., Hebert T.E., Ethier N., Bailey M., Metters K., Abramowitz M., O'Neill G.P., Ng G.Y.K.;
 RT "Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B)) receptors with truncated receptors and metabotropic glutamate receptor 4 supports the GABA(B) heterodimer as the functional receptor."
 RT J. Pharmacol. Exp. Ther. 293:460-467(2000).
 RN [9]
 RP FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY, STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS, INACTIVATES VOLTAGE-DEPENDENT CALCIUM CHANNELS AND MODULATES INOSTOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND ANTINOCICEPTION.
 CC -1- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO HAPPEN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER

CC ADDITIONAL MEMBRANE PROXIMAL SITE OF CLEAVAGE AFFECTS A SMALL
CC PERCENTAGE OF THE PROTEIN AND RESULTS IN DISULFIDE-LINKED
CC FRAGMENTS. THE PRO-DOMAIN IS APPARENTLY CLEAVED IN SEVERAL
CC POSITIONS THAT ARE N-TERMINAL OF THE FURIN CLEAVAGE SITE.
CC -1- PTM: MAY BE PARTIALLY SIALYLATED.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DISINTEGRIN DOMAIN.
CC -----
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CC -----
DR EMBL: AF006196; AAC61896.1; -
DR EMBL: AB022089; BAA88903.1; -
DR HSSP: P17494; 1KST.
DR MEROPS: M12.215; -
DR MGD: MGI:133882; Adam15.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001818; Matrxin.
DR InterPro: IPR002870; Pep_M12B_propep.
DR InterPro: IPR001590; Rep_M12B.
DR InterPro: IPR000130; Zn_MMPpeptase.
DR Pfam: PF00200; disintegrin.1.
DR Pfam: PF01421; Repolysin.1.
DR Pfam: PF01562; Pep_M12B_propep.1.
DR Pfam: PD000664; Disintegrin.1.
DR SMART: SM00050; DISIN.1.
DR SMART: SM00181; EGF.1.
DR PROSITE: PS500215; ADAM_MEROPS.1.
DR PROSITE: PS000022; EGF_1; FALSE_NEG.
DR PROSITE: PS01186; EGF_2.1.
DR PROSITE: PS00427; DISINTEGRIN_1; FALSE_NEG.
DR PROSITE: PS00424; DISINTEGRIN_2.1.
DR PROSITE: PS00142; ZINC_PROTEASE.1.
DR PROSITE: PS00546; CYSTEINE_SWITCH; FALSE_NEG.
KM Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
FT Transmembrane; EGF-like domain; SH3-binding.
FT SIGNAL 1 17
FT PROPEP 18 207
FT CHAIN 208 815
FT DOMAIN 208 696
FT TRANSMEM 697 717
FT DOMAIN 718 815
FT DOMAIN 208 415
FT DOMAIN 422 509
FT DOMAIN 510 657
FT DOMAIN 658 686
FT DOMAIN 699 712
FT SITE 767 773
FT SITE 802 808
FT SITE 179 288
FT SITE 287 288
FT METAL 349 349
FT METAL 350 350
FT ACT_SITE 350 350
FT METAL 353 353
FT METAL 359 359
FT METAL 324 410
FT DISULFID 481 494
FT DISULFID 658 668
FT DISULFID 662 674
FT DISULFID 676 685
FT CARBOHYD 238 238
FT CARBOHYD 390 390
FT CARBOHYD 393 393
FT CARBOHYD 607 607
FT CARBOHYD 612 612
FT CONFLICT 21 22

FT CONFLICT 443 443 E -> Q (IN REF. 2).
FT CONFLICT 459 459 G -> E (IN REF. 2).
FT CONFLICT 564 565 SP -> T (IN REF. 2).
FT CONFLICT 654 654 G -> E (IN REF. 2).
FT CONFLICT 660 660 R -> S (IN REF. 2).
FT CONFLICT 703 703 L -> R (IN REF. 2).
FT CONFLICT 712 712 L -> R (IN REF. 2).
FT CONFLICT 729 729 L -> R (IN REF. 2).
FT CONFLICT 797 797 L -> S (IN REF. 2).
FT CONFLICT 803 805 PAP -> AAS (IN REF. 2).
FT CONFLICT 810 810 A -> P (IN REF. 2).
FT SEQUENCE 815 AA; 87424 MW; C064BD3B7347D19B CRC64;
Query Match 7.38; Score 89; DB 1; Length 815;
Best Local Similarity 23.7%; Pred. No. 3.2;
Matches 52; Conservative 13; Mismatches 56; Indels 98; Gaps 9;
QY 69 KHKALMSFLAQWIMQKLVAGSKMOTLEDVNTIHFVTSCTPP-----LP----- 118
Db 530 KQCSLWG-----PGAQPAAPDLQIQTANTGNMFGSCGRSPGSGSYMPCAPRV 577
QY 119 -----EC-----LRFVQTNISHLKDTCTQ-----LLALK----- 143
Db 578 MCGQLQCGWGRSPPLDLSVQDRLESEVLEANGTOLNCMWVDLDGNDVAQPLALPGTAG 637
QY 144 ---PCIGKACQ-----NSRCLEVCQDPSSITLPPRSPIAL 177
Db 638 PGLVCIQHRCQPVLDLGAQECRRKCHGVODSSGHCRCGEWAPDPQMQLKATSLT 697
QY 178 EATLPEPRRQLLLLLPLTLVLLAAMGLWRORAR 216
Db 698 G-----LLSLLLLVLLGLAST---WHRAR 721
RESULT 5
AD15_RAT STANDARD; PRT; 816 AA.
ID AD15_RAT
AC Q9QYV0
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADM 15 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain 15) (metalloproteinase-like, disintegrin-like, and cysteine-rich protein 15) (MDC-15) (Metalloprotease RGD disintegrin protein)
DE rich protein 15)
DE (Metargidin) (CRII-7).
DE ADAM15 OR MDC15.
GN ADAM15 OR MDC15.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Sciatic nerve;
RX MEDLINE=20556183; PubMed=11102971;
RA Bosse F., Petzold G., Greiner-Petler R., Pipplis U., Gillen C., Mueller H.-W.;
RT "Cellular localization of the disintegrin CRII-7/rMDC15 mRNA in rat PNS and CNS and regulated expression in postnatal development and after nerve injury";
RL Gila 32:313-327(2000).
CC -1- FUNCTION: MAY BE INVOLVED IN CELL-SURFACE PROTEOLYSIS, CELL
CC ADHESION OR INTRACELLULAR PROTEIN MATURATION.
CC -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH INTEGRIN ALPHA5-BETA3, ENDOPHILIN I AND
CC SORTING NEXIN 9. ENDOPHILIN I AND SORTING NEXIN 9 PREFERENTIALLY
CC BIND THE PRECURSOR BUT NOT THE PROCESSED FORM OF ADAM15,
CC SUGGESTING THAT THE INTERACTION OCCURS IN A SECRETORY PATHWAY
CC COMPARTMENT PRIOR TO THE MEDIAL GOLGI (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I membrane protein.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN, SPINAL CORD,
CC SCIATIC NERVE AND LUNG. EXPRESSED AT LOWER LEVELS IN ALL OTHERS
CC TISSUES. IN THE PERIPHERAL NERVOUS SYSTEM, EXPRESSED PREDOMINANTLY
CC BY SCHWANN CELLS. IN THE CENTRAL NERVOUS SYSTEM, PREFERENTIALLY


```
CC -I- SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.
CC -I- CAUTION: HAS SOMETIMES BEEN REFERRED TO ADAMTS4.
CC
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CC -----
CC EMBL: AF247668; AAK28400.1; -.
CC EMBL: AB002364; BAA20821.1; -.
CC DR MEROPS: M12.220; -.
CC DR Genew: HGNC:219; ADAMTS3.
CC DR MTM, 605011; -.
CC DR InterPro: IPR001762; Disintegrin.
CC DR InterPro: IPR002870; Pep_M12B_propep.
CC DR InterPro: IPR001590; Reprolysin.
CC DR InterPro: IPR000884; TSPL.
CC DR InterPro: IPR000130; Zn_MTpeptidase.
CC DR Pfam: PF000090; tsp_1; 4_MTPeptide.
CC DR Pfam: PF01421; Reprolysin.
CC DR Pfam: PF01562; Pep_M12B_propep.
CC DR SMART: SM00209; TSPL; 4.
CC DR PROSITE: PS50215; ADAM_MERPO; 1.
CC DR PROSITE: PSS0092; TSPL; 2.
CC DR PROSITE: PS00142; ZINC_PROTEASE; FALSE NEG.
CC DR PROSITE: PS00427; DISINTEGRIN_L1; FALSE NEG.
CC KW Hydrolase; Metalloprotease; Zinc_Signal; Glycoprotein; Zymogen;
CC Repeat; Extracellular matrix; Heparin-binding.
CC FT SIGNAL 1 20 POTENTIAL.
CC FT PROPEP 21 249 BY SIMILARITY.
CC FT CHAIN 250 1205 ADAMTS-3.
CC FT METAL 398 398 ZINC (CATALYTIC) (BY SIMILARITY).
CC FT ACT_SITE 399 399 BY SIMILARITY.
CC FT METAL 402 402 ZINC (CATALYTIC) (BY SIMILARITY).
CC FT METAL 408 408 ZINC (CATALYTIC) (BY SIMILARITY).
CC FT DOMAIN 470 550 DISINTEGRIN-LIKE.
CC FT DOMAIN 551 607 TSP TYPE-1 1.
CC FT DOMAIN 608 712 CYS-RICH.
CC FT DOMAIN 713 844 SPACER.
CC FT DOMAIN 845 902 TSP TYPE-1 2.
CC FT DOMAIN 903 965 TSP TYPE-1 3.
CC FT DOMAIN 966 1017 TSP TYPE-1 4.
CC FT DOMAIN 246 249 POLY-ARG.
CC FT CARBOHD 83 83 N-LINKED (GLCNAC . . .) (POTENTIAL).
CC FT CARBOHD 119 119 N-LINKED (GLCNAC . . .) (POTENTIAL).
CC FT CARBOHD 242 242 N-LINKED (GLCNAC . . .) (POTENTIAL).
CC FT CARBOHD 345 345 N-LINKED (GLCNAC . . .) (POTENTIAL).
CC FT CARBOHD 475 475 N-LINKED (GLCNAC . . .) (POTENTIAL).
CC FT CARBOHD 814 814 N-LINKED (GLCNAC . . .) (POTENTIAL).
CC FT CARBOHD 942 942 N-LINKED (GLCNAC . . .) (POTENTIAL).
CC SO SEQUENCE 1205 AA; 135570 MW; EB07B286F85FB87 CRC64;
Query Match 6.9%; Score 84.5; DB 1; Length 1205;
Best Local Similarity 21.9%; Pred No. 12; Indels 73; Gaps 10;
Matches 49; Conservative 22; Mismatches 80;
QY 40 SNFKVKEFLDHLKLDVPYVAVALODEHCKALMSIFLAORWIEQLTVAGSK----- 94
Db 876 SDNKKVVHSFCANKPKPIRBMCIQECTH-----PLWVAEWEHCFTYCQSSGYQLRT 930
QY 95 ---MQLLEDVNTETHEFV-----TSCFFOLP-----ECLEAFV--QTNIISH 130
Db 931 VRCLOPFLDGNTRNSVSKYCMGDRPSRRRNRPVCPAPQAKGTGPMSSECVTCGEGLVEAO 990
QY 131 LL-----KDCTQLALLPCIGKAC-----QNFSRCLEVOQC 161
Db 991 VLCRAGDHODGGKPPSVARCQLPQCNDEPDFADKSLFCQMEVLARYCSLPGYNKLCCESC 1050
QY 162 QPDSTLLPRLPSIALDELTEL-----PEPRROLILLILLIP 198
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Db	1051	SKRST-LPP--PYLLEAEFTHDDVISNP5DLPPRSILVPTSLVP	1091
Qy	63	VNL0DECKKALMSLFL-----AQRWTEQLKYTAGSKM0LLIEDVNT-----	105

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Db 366 LQVDD-----LYIPDLPEPDATHLKERLKN-AINKMTMTVDNETSVTDADFGIDI 416
Oy 106 -----IHFVTC-----TFQPLPECLARVQVNIISHLKDTQTLALK 143
Db 417 DSVADVACRVAVQPFNSANVNGFSEHTRTLRLYPRVSLQDLSLRSPQCTOLIT-D 475
Oy 144 PCIGKACQNSRCLLEVOCO-PDSSTLLPPRSPALENTELEPPRPR 188
Db 476 LCRTOAVEYFAEC-----CLCPKNETFY--RVQAGIESAEQVGDKPK 515

RESULT 8
CSF1_MOUSE
ID CSF1_MOUSE STANDARD: PRT; 552 AA.
AC P07141;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Macrophage colony stimulating factor-1 precursor (CSF-1) (MCSF).
GN CSF1 OR CSF1.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090, 10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse;
RX MEDLINE=87174763; PubMed=3494232;
RA Delamarier J.F., Hession C., Semon D., Gough N.M., Rothenbuhler R.,
RA Mermod J.-J.;
RT "Nucleotide sequence of a cDNA encoding murine CSF-1
RL (Macrophage-CSF).";
RN Nucleic Acids Res. 15:2389-2390(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse;
RX MEDLINE=88320507; PubMed=2457916;
RA Lader M.B., Martin G.A., Noble J.A., Wiltman V.P., Warren M.K.,
RA McGrogan M., Stanley E.R.;
RT "cDNA cloning and expression of murine macrophage colony-stimulating
RL factor from 1929 cells.";
RN Proc. Natl. Acad. Sci. U.S.A. 85:6706-6710(1988).
RN [3]
RP SEQUENCE OF 1-100 FROM N.A.
RC SPECIES=Mouse;
RX MEDLINE=87147232; PubMed=3493488;
RA Rajavashisth T.B., Eng R., Shaddock R.K., Wahed A., Ben-Avram C.M.,
RA Shively J.E., Lusis A.J.;
RT "Cloning and tissue-specific expression of mouse macrophage colony-
RL stimulating factor mRNA.";
RN Proc. Natl. Acad. Sci. U.S.A. 84:1157-1161(1987).
RN [4]
RP SEQUENCE OF 33-57.
RC SPECIES=Mouse;
RX MEDLINE=85242709; PubMed=3925458;
RA Ben-Avram C.M., Shively J.E., Shaddock R.K., Wahed A.,
RA Rajavashisth T.B., Lusis A.J.;
RT "Amino-terminal amino acid sequence of murine colony-stimulating
RL factor 1.";
RN Proc. Natl. Acad. Sci. U.S.A. 82:4486-4489(1985).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse;
RX MEDLINE=93363632; PubMed=8357831;
RA Boyceki A.G., Lenormand J., Guillier M., Leibovitch S.A.;
RT "Isolation and characterization of a cDNA clone encoding for rat
RL CSF-1 gene. Post-transcriptional repression occurs in myogenic
RN differentiation.";
RN Biochim. Biophys. Acta 1174:143-152(1993).
RN [6]
RP SEQUENCE OF 1-13 FROM N.A.
```

```
RC SPECIES=Mouse;
RX MEDLINE=91340149; PubMed=1874443;
RA Harrington M.A., Edenberg H.J., Saxman S.M., Pedigo L.M., Daub R.,
RA Broxmeyer H.E.;
RT "Cloning and characterization of the murine promoter for the colony-
RL stimulating factor-1-encoding gene.";
RN Gene 102:165-170(1991).
CC -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
CC CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES.
CC -!- SUBUNIT: THIS CSF INDUCES MACROPHAGES.
CC -!- SUBUNIT: HOMODIMER, LINKED BY THREE DISULFIDE BONDS.
CC
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CC -----
CC EMBL; X05010; CAA28660.1; -
CC EMBL; M21952; AAA37481.1; -
CC EMBL; M21149; AAA37482.1; -
CC EMBL; M15692; AAA37480.1; -
CC EMBL; M84361; AAA3032.1; -
CC EMBL; M81316; AAA19866.1; -
CC PIR; A23166; A23166.
CC PIR; A26575; A26575.
CC PIR; A31401; A31401.
CC MGD; MGI:1339753; Csfl.
CC Cytokine; Growth factor; Glycoprotein; Signal.
CC SIGNAL
CC 1 332
CC CHAIN 33 552 MACROPHAGE COLONY STIMULATING FACTOR-1.
CC DISULFID 63 63 INTERCHAIN (BY SIMILARITY).
CC DISULFID 39 122 BY SIMILARITY.
CC DISULFID 80 171 BY SIMILARITY.
CC DISULFID 134 178 BY SIMILARITY.
CC DISULFID 189 189 INTERCHAIN (BY SIMILARITY).
CC CARBOHYD 191 191 INTERCHAIN (BY SIMILARITY).
CC CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC VARIANT 292 292 D -> G.
CC VARIANT 345 345 S -> P.
CC CONFLICT 3 3 MISSING (IN REF. 3).
CC CONFLICT 6 6 A -> R (IN REF. 3).
CC CONFLICT 246 246 AG -> PR (IN REF. 3).
CC CONFLICT 246 246 P -> A (IN REF. 1).
CC SEQUENCE 552 AA; 60648 MW; 3886D72D0E770AF CRC64;

Query Match 6.8%; Score 83.5; DB 1; Length 552;
Best Local Similarity 23.2%; Pred. No. 6.2;
Matches 54; Conservative 36; Mismatches 94; Indels 49; Gaps 12;

Oy 12 SLLILLSPCLRGPDGFSHPSSISNFKYKFEIDHLLKDPVYVAVNLQDEKH- 70
Db 18 SRLIVLLMSRSIAKEVSHCHMIGNHLKV-LQOLLDSQV-ETSCQIAFEVYQEOEL 75
Oy 71 ----CRAWLSFLAQRNTEOL-----KTVGSKMQLTLEEDVNTIEHFVTSCTFOPAP 118
Db 76 DDPVCYLKRAFLVQDIDETMRFKONTPRANITERLQELSNLN-----SCFKDYE 128
Oy 119 E-----CLR-FVQF-----NISHLKDTQTLALPCIGKACQN-FSRC--LEVQOCPD 164
Db 129 EQNKACVRFHFETPLQLEKIKNFENETKNLLEKDMNIFTKMKNNSFAKCSSRDVVTKPD 188
Oy 165 SSTLLPPRSPALENTELEPPRROLLLLLLPLTLVLVLAAMGIRGWRAR 217
Db 189 CNCLYPRATPSSDFASAPHPAP-----SWAPLA-----GLAWDSQR 228
```

RESULT 9
ZAN_PIG STANDARD: PRT: 2476 AA.
AC 028983;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Zonadhesin precursor.
GN ZAN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
[1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 823-830; 859-872; 883-890;
RP 920-925; 960-967; 1235-1244; 1349-1354; 1518-1532; 1624-1656;
RP 1658-1667; 1777-1795 AND 1914-1921.
RC STRAIN=Weishan; TISSUE=Testis;
MEDLINE=96064658; PubMed=7592795;
RA Hardy D.M., Garbers D.L.;
RT "A sperm membrane protein that binds in a species-specific manner to
the egg extracellular matrix is homologous to von Willebrand
factor";
RT J. Biol. Chem. 270:26025-26028(1995).
CC -1- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA
OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
SIGNALING.
CC -1- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE
APICAL REGION OF THE SPERM HEAD (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: IN TESTIS, PRIMARILY IN HAPLOID SPERMATIDS.
CC NOT IN LUNG, LIVER, HEART, SPLEEN, BRAIN, KIDNEY, EPIDIDYMIS.
CC -1- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE
ZONA PELLUCIDA.
CC -1- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS,
THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF
SPERMATOZOEA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.
CC -1- DOMAIN: THE VWFD DOMAINS 2 AND 3 MAY MEDIATE COVALENT
OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).
CC -1- PTM: THE MAM DOMAINS AND THE MUCIN-LIKE DOMAINS ARE MISSING
FROM THE ZONADHESIN THAT BINDS TO THE EGG EXTRACELLULAR MATRIX.
CC PROCESSING MIGHT OCCUR DURING SPERM MATURATION AND/OR
CAPACITATION.
CC -1- SIMILARITY: CONTAINS 2 MAM DOMAINS.
CC -1- SIMILARITY: CONTAINS 4.5 VWFD DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

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CC EMBL: U40024; AAC8486.1; -.
DR HSSP: P56682; ICSV.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000998; MAM_domain.
DR InterPro: IPR002919; TIL_Cysrich.
DR InterPro: IPR003328; TILA_Cysrich.
DR InterPro: IPR001007; VWF_C.
DR InterPro: IPR001846; VWF_D.
DR Pfam: PF00094; vwd; 4.
DR Pfam: PF00629; MAM; 2.
DR Pfam: PF01826; TIL; 5.
DR Pfam: PF02345; TILA; 5.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00137; MAM; 1.
DR SMART: SM00214; VWC; 2.
DR SMART: SM00216; VWD; 4.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 4.

DR PROSITE: PS00740; MAM_1; 1.
DR PROSITE: PS00600; MAM_2; 2.
KW Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion;
KW Repeat.
FT SIGNAL 1 29
FT CHAIN 30 2476
FT DOMAIN 30 2418
FT TRANSMEM 2419 2439
FT DOMAIN 2440 2476
FT DOMAIN 31 144
FT DOMAIN 147 312
FT DOMAIN 319 687
FT DOMAIN 688 799
FT DOMAIN 800 1184
FT DOMAIN 1185 1573
FT DOMAIN 1574 1968
FT DOMAIN 1969 2370
FT DOMAIN 2366 2402
FT DISULFID 2370 2381
FT DISULFID 2375 2390
FT DISULFID 2392 2401
FT CARBOHYD 109 109
FT CARBOHYD 269 269
FT CARBOHYD 735 735
FT CARBOHYD 758 758
FT CARBOHYD 833 833
FT CARBOHYD 1154 1154
FT CARBOHYD 1329 1329
FT CARBOHYD 1448 1448
FT CARBOHYD 1544 1544
FT CARBOHYD 1596 1596
FT CARBOHYD 1654 1654
FT CARBOHYD 1843 1843
FT CARBOHYD 1965 1965
FT CARBOHYD 2122 2122
FT CARBOHYD 2165 2165
FT CARBOHYD 2178 2178
FT CARBOHYD 2329 2329
FT CARBOHYD 2359 2359
FT CONFLICT 823 823
FT CONFLICT 923 923
FT CONFLICT 965 965
FT CONFLICT 1241 1241
SQ SEQUENCE 2476 AA; 270364 MW; A13B690375A6548C CRC64;

Query Match Best Local Similarity 30.6%; Score 83.5; DB 1; Length 2476;
Matches 26; Conservative 12; Mismatches 32; Indels 15; Gaps 3;

QY 144 PCIGACQNFSCLE-----VQC-----PPSSITLPPRSIALEATLEPPRRQLLL 193
DB 2369 PCLQNPCCNDGRCRGTHFTCECELGSGDLCT-----EPRGVSPKPPASNRVAILL 2423
QY 194 LLLPLPLVILAAAGLGMORARR 218
DB 2424 GMLPPTVLLVPAVTVSKRRRRR 2448

RESULT 10
LEUK_RAT
ID LEUK_RAT STANDARD: PRT: 378 AA.
AC P13838;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Leukostialin precursor (leucocyte sialoglycoprotein) (Sialophorin)
DE (CD43) (W3/13 antigen) (Fragment).
GN SPN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-THYMOCYTES;
RX MEDLINE-816646; PubMed-2965006;
RA Killen N., Barclay A.N., Willis A.C., Williams A.F.;
RT "The sequence of rat leukostallin (w3/13 antigen) reveals a molecule
RT with O-linked glycosylation of one third of its extracellular amino
RT acids."
RL EMBL J. 6:4029-4034(1987).
CC -1- FUNCTION: ONE OF THE MAJOR GLYCOPROTEINS OF THYMOCYTES AND T
CC LYMPHOCYTES. PLAYS A ROLE IN THE PHYSICO-CHEMICAL PROPERTIES OF
CC THE T-CELL SURFACE AND IN LECTIN BINDING. PRESENTS CARBOHYDRATE
CC LIGANDS TO SELECTINS. HAS AN EXTENDED RODLIKE STRUCTURE THAT COULD
CC PROTRUDE ABOVE THE GLYCOALYX OF THE CELL AND ALLOW MULTIPLE
CC GLYCAN CHAINS TO BE ACCESSIBLE FOR BINDING.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: CELL SURFACE OF THYMOCYTES, T LYMPHOCYTES,
CC NEUTROPHILS, PLASMA CELLS AND MYELOMAS.
CC -1- PTM: HAS A HIGH CONTENT OF SIALIC ACID AND O-LINKED CARBOHYDRATE
CC STRUCTURES.
CC -----
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CC -----
DR EMBL; Y00090; CA68281.1;
DR PIR; S00842; S00842.
KW Glycoprotein; Transmembrane; signal; T-cell; Antigen.
FT NON_TER 1 7
FT SIGNAL 1 7
FT CHAIN 8 378
FT DOMAIN 8 231
FT TRANSMEM 232 254
FT DOMAIN 255 378
FT CARBOHYD 13 13
FT CARBOHYD 15 15
FT CARBOHYD 20 20
FT CARBOHYD 23 23
FT CARBOHYD 25 25
FT CARBOHYD 27 27
FT CARBOHYD 28 28
FT CARBOHYD 29 29
FT CARBOHYD 33 33
FT CARBOHYD 34 34
FT CARBOHYD 36 36
FT CARBOHYD 37 37
FT CARBOHYD 40 40
FT CARBOHYD 108 108
FT CARBOHYD 113 113
FT CARBOHYD 118 118
FT CARBOHYD 120 120
FT CARBOHYD 124 124
FT CARBOHYD 125 125
FT CARBOHYD 126 126
FT CARBOHYD 174 174
FT CARBOHYD 176 176
FT CARBOHYD 180 180
FT CARBOHYD 183 183
FT CARBOHYD 187 187
FT CARBOHYD 189 189
FT SEQUENCE 378 AA; 38425 MW; 231C808BA8A257C CRC64;
OY 9 SPNSLLILLILLSPCLGTPDC--YFSHSPISNFKVKKRELT----- 50
DB 59 APASSIPL-----GTEPLSSFFFTTSAGASGNTPVP--ELTTSQEVSTEASLVLP 106

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OY 51 --DHLIKDPTVAVNLODEKCKALMSLELAQRMIEQLKTVAAGSKMOTLLEDVNTETIHF 108
DB 107 KSSGVADEPPVIT-----NPATSSAAVASTLEFFKGTSAAPPV----- 145
OY 109 YVSCTFQPLPELRLPVQTNIS-----HLIKPTCOLLAKPCIG 147
DB 146 VTSSTMTSGP-----FVANTVSSETSGPPVMTATGSLGSKETHGLSATIATVSSGESSVA 201
OY 148 KACQNFSCLEVCOPDSSTLLPPRSPIALBATELPEPRPROLLILLPLPTVLLAA 207
DB 202 GSTPVEFTKISTSPNPNTITVPPR-----PGSSGMLVSLMILATVIVLVVA 249
OY 208 WCLRW-QRARR 218
DB 250 LLLMRQRKR 261
RESULT 11
APA4_MOUSE
ID APA4_MOUSE STANDARD; PRT; 395 AA.
AC P06728;
DT 01-JAN-1988 (Rel. 06, Created)
DI 01-OCT-1996 (Rel. 34, last sequence update)
DE 15-DEC-1998 (Rel. 37, last annotation update)
DE Apolipoprotein A-IV precursor (Apo-AIV).
GN APOA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-67089722; PubMed-3796595;
RA Williams S.C., Bruckheimer S.M., Lusis A.J., LeBoeuf R.C.,
RA Kinlburgh A.J.;
RT "Mouse apolipoprotein A-IV gene: nucleotide sequence and induction by
RT a high-lipid diet";
RL Mol. Cell. Biol. 6:3807-3814(1986).
RN [2]
RP REVISIONS.
RA Kinlburgh A.J.;
RL submitted (DEC-1986) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-C57BL/6J; and 129/J;
RX MEDLINE-91286309; PubMed-1648102;
RA Reue K., Leete T.H.;
RT "Genetic variation in mouse apolipoprotein A-IV due to insertion and
RT deletion in a region of tandem repeats.";
RL J. Biol. Chem. 266:12715-12721(1991).
CC -1- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
CC CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
CC LIPIASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
CC COMPONENT OF HDL AND CHYLOMICRONS.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: SECRETED IN PLASMA.
CC -1- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
CC 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-
CC MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
CC HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECTITHIN:CHOLESTEROL
CC ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
CC -1- POLYMORPHISM: THERE IS A POLYMORPHISM WITHIN A SERIES OF IMPERFECT
CC REPEATS ENCODING THE SEQUENCE E-Q-[AV]-Q. INSERTIONS OR DELETIONS
CC OF 12 NUCLEOTIDES HAVE GIVEN RISE TO THREE FORMS CHARACTERIZED BY
CC THREE (129), FOUR (C57BL/6), OR FIVE (M.CASTANEUS) COPIES OF THE
CC REPEAT UNIT.
CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
CC -----
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QY 13 SLILLILLSPCLRGTPDCYFSHSP---ISSNFKV--KPEELTDH----- 52
Db 6 SLRMALVLYSCPGSGCYLSRPLTDVRENRLDRMRRLSPHSGQDRKFGLPQEM 65
QY 53 -----LLKDYPRVY-----AVNLDEKCKALMSLEFLAORMIEOLKTVAGSKMOTLLE 100
Db 66 VEGDLOKLDALSVLYEMLOQRFNLFHTETHSCAAMNTTL-----LEQIRF--GLHQO--LE 117
QY 101 DVNT 104
Db 118 DEDT 121

RESULT 13
YAAG_SCHPO STANDARD; PRT; 1101 AA.
AC 009733;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C31A2.16 in chromosome I.
CN SPAC31A2.16
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Scouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howard S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Miblett D., Ocell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Stevens K., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grynoprez B.,
RA Wellens J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -1- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY (DH) DOMAIN.
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CC
CC EMBL: Z50113; CAA90474.1; -
CC InterPro: IPR001331; GDS_CDC24.
CC InterPro: IPR000219; RhogEF.
CC Pfam: PF00621; RhogEF; 1.
CC SMART: SM00325; RhogEF; 1.

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DR PROSITE: PS00741; DH 1; FALSE_NEG.
DR PROSITE: PS50010; DH 2; 1.
KW Hypothetical protein.
RT DOMAIN 230 428 DH.
SQ SEQUENCE 1101 AA; 126537 MW; B26C47589676F50B CRC64;
Query Match 6.5%; Score 79; DB 1; Length 1101;
Best Local Similarity 20.0%; Pred. No. 33;
Matches 42; Conservative 32; Mismatches 66; Indels 70; Gaps 8;
QY 37 PISNFKVFKRELTDHLKD-----YPTVAVNLDEKCKAL---WSFLAQRW 83
Db 815 PLSEKEKIEGDELVDNILEKTFNEELLISHYPPNI-IVATFQKYLSSFNKKFVLLSSSF 873
QY 84 IEOLKTVAGSKMOTLLEPVN-----TEIHFTSCFOPLECLRFVQTNISHLKDCQTO 138
Db 874 IQQLNTV-----ENLNLSFNSTDVYHLKILQDLPPSSUKILENIFSIASD----- 920
QY 139 LIALKPCIGKACQNFRCLEVOQCPDS-----STLLPPRSPI 175
Db 921 -LLRLPLKDDQDPYTKQALATALAPSMFGSNAVELVYLAHSRIGTVBELPTPVSPA 979
QY 176 -----ALEATELPEPRROL 191
Db 980 NSNDKQLEDSKFKQAIAMKEMPERHPRKEL 1009

RESULT 14
YW72_MYCTU STANDARD; PRT; 122 AA.
AC 050691;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein RV2272.
GN RV2272 OR MT2333 OR MYC339.38C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaua F.,
RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: TO E COLI YIDH.
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DR EMBL: 277163; CAB00963.1;
DR EMBL: AE007076; AAK46616.1;
DR TIGR: MT2333;
DR Tuberculosis; Ry2272;
DR InterPro: IPR003807; DUF202.
DR Pfam: PF02656; DUF202; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 33 53 POTENTIAL.
FT TRANSMEM 58 78 POTENTIAL.
FT TRANSMEM 97 117 POTENTIAL.
SQ SEQUENCE 122 AA; 12994 MW; 23a53754264887a7 CRC64;

Query Match
Best local Similarity 33.0%; Pred. No. 3.1; Length 122;
Matches 29; Conservative 12; Mismatches 24; Indels 23; Gaps 5;

QY 162 QDP-STLPPRSPALAEAT-----ELPEPRRQILLILLPLTVLL 204
DB 13 EPDYRETLNERFTFLMOWTALGLAAAVLVOLVPELTIPGARQYLGVALI---LAIL 69
QY 205 AAAMG-LRMORARRRGEIHPGVLPSPHP 231
DB 70 TSGMGLRMQADRAMRRH--LPSPHP 95

RESULT 15
RC04 HUMAN STANDARD; PRT; 1208 AA.
NC 094761;
DT 30-MAY-2000 (Rel. 39, Created)
DT 15-JUN-2002 (Rel. 39, Last sequence update)
DE ATP-dependent DNA helicase Q4 (Reco protein-like 4).
GN RECO4 OR RECO4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=90907344; PubMed=9878247;
RA Kito S., Ohsugi I., Ichikawa K., Goto M., Furuchi Y., Shimamoto A.;
RT "Cloning of two new human helicase genes of the Reco family:
RT biological significance of multiple species in higher eukaryotes.";
RT Genomics 54:443-452(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20021764; PubMed=10552928;
RA Kito S., Lindor N.M., Shiratori M., Furuchi Y., Shimamoto A.;
RT "Rothmund-Thomson syndrome responsible gene, RECO4: genomic structure
RT and products.";
RT Genomics 61:268-276(1999).
RC [1] SUBCELLULAR LOCATION: Nuclear (Potential).
CC [1] DISEASE: DEFECTS IN RECO4 ARE A CAUSE OF ROTHMUND-THOMSON
CC SYNDROME (RTS). A DISEASE CHARACTERIZED BY DERMATOLOGICAL FEATURES
CC SUCH AS ATROPHY, PIGMENTATION, AND TELANGIECTASIA AND FREQUENTLY
CC DEFECTS, DISTURBANCES OF HAIR GROWTH, AND HYPOGONADISM.
CC [1] SIMILARITY: BELONGS TO THE HELICASE FAMILY. RECO SUBFAMILY.
CC [1] DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chromancer/Genes/RECO4ID285.html".
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR EMBL: AB006532; BAA74453.1;
DR EMBL: AB026546; BAA68899.1;
DR Genem: HGNC:9949; RECO4.
DR MIM: 603780;
DR MIM: 268400;
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR004589; Reco.
DR InterPro: IPR001878; ZnF_CCHC.
DR Pfam: PF00270; DEAD; 1.
DR Pfam: PF00271; Helicase_C; 1.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELIC; 1.
DR SMART: SM00343; ZnF_C2HC; 1.
DR TIGRFAMs: TIGR00614; recQ; 1.
KW Hydrolyase; Helicase; ATP-binding; Nuclear protein.
FT NP_BIND 502 509 ATP (POTENTIAL).
FT SITE 605 608 DEAD BOX.
SQ SEQUENCE 1208 AA; 133076 MW; CB809A7765AB48A1 CRC64;

Query Match
Best local Similarity 22.8%; Score 78.5; DB 1; Length 1208;
Matches 66; Conservative 27; Mismatches 111; Indels 85; Gaps 13;

QY 9 SPNSLTL-LLLLSPLCTRGTPDCYS---HSPIS---SNFKVRFRELDHLLKDPV 59
DB 523 SPCLTLVSPPLSLMDQVSGLPCLAKACIHSGMTKGRSVLQKTRAQVHYLMITPE 562
QY 60 T-----VAVNIQDERHCKALMSFLAQRWIEQLKV----- 90
DB 583 ALVAGAGLPAAQLPPVAFACIDEAHCLISQWSHNFRCYLRCVKLBERMGVHCFGLTA 642
QY 91 -----AGSKMOTLEDVNTETIHVTSCTFQPLRECLRFYQTNISHL-----KDTGQL 140
DB 643 TATRTTASDVQAQHLVAEEDPLH-----GPAP-----VPTN-LHLSVMSDRTDQALL 669
QY 141 ALKPCIGKACQNF-----RCLEVOCQPPSSTLLPPRSPALAEAT 180
DB 690 TLLQ--GKRFQNDLSIIYYCRREDTERIALLTCLHAAMVPPSGGRAKRTTAETAHAG 747
QY 181 ELPEPRRQILLILLPLTVLLAAAMGLRMORARRRGEIHPGVLPSP 229
DB 748 MCSRRR-RRVQRAFMQGLRVVAVTAVFGMGLDRPDVRAVLHLGLP-PS 794

Search completed: November 24, 2002, 10:10:43
Job time : 12.427 secs
```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 24, 2002, 10:08:21 ; Search time 25.7766 Seconds
(without alignments)
1846.499 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223
Sequence: 1 MTVALPAPMSPNSLLILL.....WQARRRGELHPGVLPSPHP 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP:archaea:*
2: SP:bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-virus:*
16: SP-bacteriaph:*
17: SP-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	879	71.9	172	11 061104	061104 mus musculus
2	842.5	68.9	169	11 08VCH4	08VCH4 mus musculus
3	779.5	63.7	292	6 09GKE0	09GKE0 bos taurus
4	774.5	63.3	292	6 08BNW1	08BNW1 bos taurus
5	774	63.3	294	6 09MZV0	09MZV0 canis fam11
6	761	62.2	291	6 09MKD9	09MKD9 felis silve
7	678.5	55.5	274	6 09GKD9	09GKD9 bos taurus
8	95.5	7.8	909	10 042484	042484 arabidopsis
9	94	7.7	355	4 09H665	09H665 homo sapien
10	93.5	7.6	510	6 09BGY6	09BGY6 macaca fasc
11	90.5	7.4	909	10 09ASPS	09ASPS arabidopsis
12	88.5	7.2	326	12 083443	083443 murine rota
13	88.5	7.2	326	12 083448	083448 murine rota
14	88	7.2	258	4 09H563	09H563 homo sapien
15	88	7.2	765	4 094824	094824 homo sapien
16	88	7.2	843	4 014584	014584 homo sapien

17	88	7.2	1028	5 08SXA6	08SXA6 drosophila
18	88	7.2	1254	5 09VFS1	09VFS1 drosophila
19	87.5	7.2	477	11 09CYB2	09CYB2 mus musculus
20	87.5	7.2	1231	10 09FKE2	09FKE2 arabidopsis
21	87	7.1	291	16 08ZAH9	08ZAH9 yersinia pe
22	87	7.1	1256	5 09VFS0	09VFS0 drosophila
23	86.5	7.1	2111	5 091802	091802 drosophila
24	86.5	7.1	4167	5 09GPN8	09GPN8 drosophila
25	86	7.0	962	5 096164	096164 plasmodium
26	85	7.0	181	5 017726	017726 caenorhabd1
27	85	7.0	1305	2 006521	006521 enterococcu
28	85	7.0	4513	10 09MBF8	09MBF8 chlamydomon
29	84.5	6.9	364	4 096AY5	096AY5 homo sapien
30	84.5	6.9	939	16 09KOC8	09KOC8 vltrio chol
31	84	6.9	330	5 09N4U7	09N4U7 caenorhabd1
32	83.5	6.8	588	8 09B6D1	09B6D1 yarrowia 11
33	83	6.8	258	4 09UMT2	09UMT2 homo sapien
34	83	6.8	267	5 09W2D7	09W2D7 drosophila
35	83	6.8	341	5 08T0N4	08T0N4 drosophila
36	83	6.8	1059	5 09VNP5	09VNP5 drosophila
37	82.5	6.7	326	12 085032	085032 porcine rot
38	82.5	6.7	326	12 085034	085034 porcine rot
39	82.5	6.7	335	8 09ZY32	09ZY32 orycterus
40	82.5	6.7	379	8 09T7T9	09T7T9 taptirus ind
41	82.5	6.7	431	10 09SN38	09SN38 arabidopsis
42	82.5	6.7	809	11 09DBY4	09DBY4 mus musculus
43	82.5	6.7	1266	10 09XET3	09XET3 lycopersico
44	82	6.7	575	10 09LS68	09LS68 arabidopsis
45	81.5	6.7	659	4 09H9U7	09H9U7 homo sapien

ALIGNMENTS

RESULT 1

ID	061104	PRELIMINARY:	PRT:	172 AA.
AC	061104;			
DT	01-NOV-1996 (TREMblrel. 01, Created)			
DT	01-NOV-1996 (TREMblrel. 01, Last sequence update)			
DT	01-JUN-2002 (TREMblrel. 21, Last annotation update)			
DE	Flt3 ligand, T169 form.			
GN	FLT3L.			
OS	Mus musculus (Mouse).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	McClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Bacon K.,			
RA	Mattson J., Tsai S., Luh J., Guimares M.J., Mattel M.-G., Rosnet O.,			
RA	Birnbaum D., Hannum C.;			
RT	"Flt3 ligand: expression, genomic organization, alternatively spliced			
RT	forms and processing."			
RL	Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; U44024; AAA93305.1; -			
DR	MGI; MGI:95560; FLT3L.			
DR	InterPro; IPR004213; Flt3_lig.			
DR	InterPro; IPR001230; Prenyl_site.			
DR	Pfam; PF02947; Flt3_lig.1.			
DR	PROSITE; PS00294; PRENYLATION; UNKNOWN.1.			
SO	SEQUENCE 172 AA; 19465 MW; 04FOA01017E3384 CRC64;			

Query Match Best Local Similarity 71.9%: Score 879; DB 11: Length 172;

Matches 165; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MTVALPAPMSPNSLLILLSPCLRGTPDCYFSHSPSSNFYKFRRLDHLKDPVT 60		
Db	1	MTVALPAPMSPNSLLILLSPCLRGTPDCYFSHSPSSNFYKFRRLDHLKDPVT 60		
Qy	61	VAVNIQDKKCKALMSFLAQRWIEOLKTVAGSKMOTLLEDVNTETTFVNSCTFQPLPEC 120		

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Db 61 VAVNLQDEKHKALMSFLAQRWIEOLKTAVAGSKMOTLLEVDNTEIHFTVTSCTFOPLPEC 120
QY 121 LRFVQTNISHLKDTCTQTLALKPCIGKACONFSRCLEVOCCOPDSSPTL 168
    |||||
Db 121 LRFVQTNISHLKDTCTQTLALKPCIGKACONFSRCLEVOCCOPDSSPTL 168

RESULT 2
Q8VCH4
ID 08VCH4 PRELIMINARY; PRT; 169 AA.
AC 08VCH4;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to FMS-like tyrosine kinase 3 ligand.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver.
RA Strausberg R.;
RL EMBL; BC019801; AA019801.1; -.
DR InterPro: IPR004213; Flt3_lig.
DR Pfam: PF02947; flt3_lig; 1.
KW Kinase.
SQ SEQUENCE 169 AA; 18986 MW; 5B4CA7D9724EFF2 CRC64;

Query Match 68.9%; Score 842.5; DB 11; Length 169;
Best Local Similarity 92.5%; Pred. No. 7.7e-78;
Matches 161; Conservative 0; Mismatches 4; Indels 9; Gaps 1;

QY 1 MTVLAPAMSPNSLLILLISPCIRGTPDCYFSHPSSISNFKYKRELTDHLKDPVT 60
Db 1 MTVLAPAMSPNSLLILLISPCIRGTPDCYFSHPSSISNFKYKRELTDHLKDPVT 60
QY 61 VAVNLQDEKHKALMSFLAQRWIEOLKTAVAGSKMOTLLEVDNTEIHFTVTSCTFOPLPEC 120
    |||||
Db 61 VAVNLQDEKHKALMSFLAQRWIEOLKTAVAGSKMOTLLEVDNTEIHFTVTSCTFOPLPEC 120
QY 121 LRFVQTNISHLKDTCTQTLALKPCIGKACONFSRCLEVOCCOPDSSPTLPPRSP 174
    |||||
Db 121 LRFVQTNISHLKDTCTQTLALKPCIGKACONFSRCLEVOCCOPDSSPTLPPRSP 174

RESULT 3
Q8GKEO
ID 08GKEO PRELIMINARY; PRT; 292 AA.
AC 08GKEO;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Flt3 ligand isoform-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20570936; PubMed=11120823;
RA Mwangi W., Brown W.C., Palmer G.H.;
RT "Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain
RT required for receptor binding and function using naturally occurring
RT ligand isoforms."
RL J. Immunol. 165:6966-6974(2000).
DR EMBL; AF282985; AAF93322.1; -.
DR InterPro: IPR004213; Flt3_lig.
DR Pfam: PF02947; flt3_lig; 1.
SQ SEQUENCE 292 AA; 32390 MW; D6B89ED79221202D CRC64;

```

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Query Match 63.7%; Score 779.5; DB 6; Length 292;
Best Local Similarity 62.8%; Pred. No. 3.7e-71;
Matches 165; Conservative 20; Mismatches 43; Indels 33; Gaps 5;

QY 1 MTVLAPAMSPNSLLILLISPCIRGTPDCYFSHPSSISNFKYKRELTDHLKDPVT 60
    |||||
Db 1 MTVLAPAMSPNSLLILLISPCIRGTPDCYFSHPSSISNFKYKRELTDHLKDPVT 60
QY 61 VAVNLQDEKHKALMSFLAQRWIEOLKTAVAGSKMOTLLEVDNTEIHFTVTSCTFOPLPEC 120
    |||||
Db 61 VAVNLQDEKHKALMSFLAQRWIEOLKTAVAGSKMOTLLEVDNTEIHFTVTSCTFOPLPEC 120
QY 121 LRFVQTNISHLKDTCTQTLALKPCIGKACONFSRCLEVOCCOPDSSPTLPPRSP 180
    |||||
Db 121 LRFVQTNISHLKDTCTQTLALKPCIGKACONFSRCLEVOCCOPDSSPTLPPRSP 180
QY 121 LRFVQTNISHLKDTCTQTLALKPCIGKACONFSRCLEVOCCOPDSSPTLPPRSP 180
    |||||
Db 121 LRFVQTNISHLKDTCTQTLALKPCIGKACONFSRCLEVOCCOPDSSPTLPPRSP 180
QY 181 ELPEPR-PROLILLILLPLTVLLAAWGL-RWQARRR----- 218
    |||||
Db 179 SLPGQSPDLLILLIPVALLATATWCLCRRRRRRRTYRPGERRRTLRPRESSHLPA 238
    |||||
QY 219 -----GELHGVPLPSHP 231
    |||||
Db 239 DTESLGSQLEPG-PFLGHP 258

RESULT 4
Q8NMN1
ID 08NMN1 PRELIMINARY; PRT; 292 AA.
AC 08NMN1;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Flt3 ligand.
GN Flt3 LIGAND.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Hikono H., Komotani E.;
RT "Cloning of a cDNA for bovine flt3 ligand."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051841; BAB79634.1; -.
DR InterPro: IPR004213; Flt3_lig.
DR Pfam: PF02947; flt3_lig; 1.
SQ SEQUENCE 292 AA; 32388 MW; 2A797E0C1199C1D9 CRC64;

Query Match 63.3%; Score 774.5; DB 6; Length 292;
Best Local Similarity 62.8%; Pred. No. 1.2e-70;
Matches 164; Conservative 20; Mismatches 44; Indels 33; Gaps 5;

QY 1 MTVLAPAMSPNSLLILLISPCIRGTPDCYFSHPSSISNFKYKRELTDHLKDPVT 60
    |||||
Db 1 MTVLAPAMSPNSLLILLISPCIRGTPDCYFSHPSSISNFKYKRELTDHLKDPVT 60
QY 61 VAVNLQDEKHKALMSFLAQRWIEOLKTAVAGSKMOTLLEVDNTEIHFTVTSCTFOPLPEC 120
    |||||
Db 61 VAVNLQDEKHKALMSFLAQRWIEOLKTAVAGSKMOTLLEVDNTEIHFTVTSCTFOPLPEC 120
QY 121 LRFVQTNISHLKDTCTQTLALKPCIGKACONFSRCLEVOCCOPDSSPTLPPRSP 180
    |||||
Db 121 LRFVQTNISHLKDTCTQTLALKPCIGKACONFSRCLEVOCCOPDSSPTLPPRSP 180
QY 121 LRFVQTNISHLKDTCTQTLALKPCIGKACONFSRCLEVOCCOPDSSPTLPPRSP 180
    |||||
Db 121 LRFVQTNISHLKDTCTQTLALKPCIGKACONFSRCLEVOCCOPDSSPTLPPRSP 180
QY 181 ELPEPR-PROLILLILLPLTVLLAAWGL-RWQARRR----- 218
    |||||
Db 179 SLPGQSPDLLILLIPVALLATATWCLCRRRRRRRTYRPGERRRTLRPRESSHLPA 238
    |||||
QY 219 -----GELHGVPLPSHP 231
    |||||
Db 239 DTESLGSQLEPG-PFLGHP 258

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RESULT 5

Q9MZV0

PRELIMINARY: PRT: 294 AA.

AC Q9MZV0;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Flt3 ligand.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OC NCBL_Taxid=9615;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20358731; PubMed=10902925;

RA Yang S., Sim G.K.;

RT "Molecular cloning of canine and feline flt3 ligand reveals high

RT degree of similarity to the human and mouse homologue but uniquely

RT long cytoplasmic domain."

RL DNA Seq. 11:163-166(2000).

RL EMBL; AF155148; AAF87088.1; -.

DR InterPro: IPR004213; Flt3_1lg.

DR Pfam: PF02947; flt3_1lg. 1.

SQ SEQUENCE 294 AA; 32394 MW; 6859917AB74ABCD CRC64;

Query Match 63.3%; Score 774; DB 6; Length 294;

Best Local Similarity 70.2%; Pred. No. 1.3e-70;

Matches 158; Conservative 23; Mismatches 38; Indels 6; Gaps 4;

QY 1 MYVLAPAMSPNSLLDLLLSPCLRGTPDCYFSHSPISSNFVKFRELTDHLKDPVT 60

DB 1 MYVLAPAMSPPTTS-LLDLLLSPCLRGTPDCSFHSPISSNFVKFRELTDHLKDPVT 59

QY 61 VAVNLQDEKHCALMSFLAQRWIEQLKTVAAGSKMOTLEDVNTLHFTVCTFOPLPEC 120

DB 60 VASNLQDEKHCALMSFLAQRWIEQLKTVAAGSKMOTLEDVNTLHFTVCTFOPLPEC 119

QY 121 LRFVQTNISHLKTCQQLALAKPCIGKACONFSRCLEVOQCPDSSSTLLPPSPALAEAT 180

DB 120 LRFVQTNISHLKTCQQLALAKPCIGKACONFSRCLEVOQCPDSSSTLLPPSPALAEAT 177

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRRRRSPYPG 220

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRRRRSPYPG 220

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRRRRSPYPG 220

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRRRRSPYPG 220

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRRRRSPYPG 220

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRRRRSPYPG 220

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRRRRSPYPG 220

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRRRRSPYPG 220

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRRRRSPYPG 220

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRRRRSPYPG 220

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRRRRSPYPG 220

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRRRRSPYPG 220

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRRRRSPYPG 220

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRRRRSPYPG 220

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRRRRSPYPG 220

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRRRRSPYPG 220

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRRRRSPYPG 220

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRRRRSPYPG 220

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRRRRSPYPG 220

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRRGEIHPG 224

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRRRRSPYPG 220

Best Local Similarity 71.1%; Pred. No. 2.8e-69;

Matches 155; Conservative 22; Mismatches 37; Indels 4; Gaps 3;

QY 1 MYVLAPAMSPNSLLDLLLSPCLRGTPDCYFSHSPISSNFVKFRELTDHLKDPVT 60

DB 1 MYVLAPAMSPPTTS-LLDLLLSPCLRGTPDCSFHSPISSNFVKFRELTDHLKDPVT 59

QY 61 VAVNLQDEKHCALMSFLAQRWIEQLKTVAAGSKMOTLEDVNTLHFTVCTFOPLPEC 120

DB 60 VASNLQDEKHCALMSFLAQRWIEQLKTVAAGSKMOTLEDVNTLHFTVCTFOPLPEC 119

QY 121 LRFVQTNISHLKTCQQLALAKPCIGKACONFSRCLEVOQCPDSSSTLLPPSPALAEAT 180

DB 120 LRFVQTNISHLKTCQQLALAKPCIGKACONFSRCLEVOQCPDSSSTLLPPSPALAEAT 177

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

QY 181 ELPEPR-PROLLLLLLPLTLVLLAAAGLFWORARRR 218

DB 178 ALPAPQAPR-LLLLLLPLVALLMLSTAMCLHWRRRRR 214

ID	042484	PRELIMINARY:	PRT:	909 AA.
DT	01-NOV-1996 (TREMblrel_01, Created)			
DT	01-NOV-1996 (TREMblrel_01, Last sequence update)			
DT	01-JUN-2002 (TREMblrel_21, Last annotation update)			
DE	Rps2 (Disease resistance protein RPS2).			
GN	Rps2 OR F20B18.200 OR At4G26090.			
OC	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota: Viridiplantae: streptophyta: Embryophyta: Tracheophyta:			
OC	Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:			
OC	eurosid II: Brassicales: Brassicaceae: Arabidopsis.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=COL-0;			
RX	MEDLINE=94377978; PubMed=8091210;			
RA	Bent A.F., Kunkel B.N., Dahlbeck D., Brown K.L., Schmidt R.,			
RA	Giraudat J., Leung J., Shalkawitz B.J.;			
RT	"RPS2 of Arabidopsis thaliana: a leucine-rich repeat class of plant			
RL	disease resistance genes.";			
RL	Science 265:1856-1860(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9500758; PubMed=7923358;			
RA	Mandrinis M., Katagiri F., Yu G., Ausubel F.M.;			
RT	"The A. thaliana disease resistance gene RPS2 encodes a protein			
RL	containing a nucleotide-binding site and leucine-rich repeats.";			
RL	Cell 78:1089-1099(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Beyan M., Rose M., Hempel S., Entian K.-D., Hohnel J., Mewes H.W.,			
RA	Mayer K.F.X., Schneller C.;			
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	EU Arabidopsis sequencing project;			
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K.,			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RP	[6]			
RP	SEQUENCE FROM N.A.			
RA	EU Arabidopsis sequencing project;			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: U1158: AAA21874.1; -;			
DR	EMBL: U12860: AAA50236.1; -;			
DR	EMBL: AL049483: CAB39674.1; -;			
DR	EMBL: AL161564: CAB79464.1; -;			
DR	InterPro: IPR000767; Disease_resist.			
DR	InterPro: IPR001611; LRR.			
DR	InterPro: IPR002182; NB-ARC.			
DR	Pfam: PF00560; LRR; 4.			
DR	Pfam: PF00931; NB-ARC; 1.			
DR	PRINTS: PR00364; DISEASESIST.			
DR	SEQUENCE 909 AA; 104640 MW; D279B6E30E49D640 CRC64;			

[illegible]

QY	149	ACONSTRCELEVOCCPDSSTLPPSPPLAETETPEERPRROLILLILLPLUTVLAAAN	208
Db	715	HERNRR-LSTKSCHDELYV---TPADFEENDWLPs---LEVTLHSLHNLTRV-----W	7623
QY	209	G 209	
Db	763	G 763	
RESULT 9			
ID	Q9H665	PRELIMINARY;	PRT; 355 AA.
AC	Q9H665;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)		
DE	CIDNA: FLJ22573 f1s, clone HS102387.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=SMALL INTESTINE;		
RA	Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,		
RA	Suzuki Y., Odayashi M., Nishi T., Shibahara T., Tanaka T.,		
RA	Nakamura Y., Isono T., Sugano S.;		
RT	"NEDO human cDNA sequencing project."		
RL	submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AK026226; BAB15400.1.		
SQ	SEQUENCE 355 AA; 37894 MW; 52CA17A3E6736623C CRC64;		

```

Query Match= 7.7% Score 94; DB 4; Length 355;
Best Local Similarity 20.6% Pred No. 0.25;
Matches 41; Conservative 15; Mismatches 59; Indels 84; Gaps 6;

Qy 116 PLPE---CLRFVQTNISHLKDTQTLLAKPC---IGKAC-----QNSRCL 157
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 18 PPPEASQYCGRLFEWYMDPNKCCSCLQRRGPPCPDYEFRENCGLNDHGDVTPPFKCS 77
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 158 EVCCQPDSSSLPLP----- 171
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 78 SGQGNPFGAELCSPCGGAVTPTPAAGGGRTPWRCREPRVPKAGCHPLTGNPGAPSSGE 137
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 172 -RSPLEALEATLEPPRP-----LTLTLTLPLTVLAAAMGRMORARGE 220
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 138 RSSASSIAKRTPEPPQQAENRLEPLVYVLLTLVAILLEITLIMHLCWKEKADPY 197
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 221 LHPGV-----PLPSH 230
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 198 PYPGLVCGVPNTHTPSSSH 216
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
Q9BGY6 PRELIMINARY; PRT; 510 AA.
O9BGY6
AC O9BGY6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 56.5 kDa protein.
OS Macaca fascicularis (Craib eating macaque) (Cynomolgus monkey).
EC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
CX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FRONTAL LOBE LEFT;
RA Oosada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
   libraries.";
```

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB055271; BAB21895.1; -
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR003592; LRR_out.
 DR InterPro: IPR003591; LRR_typ.
 DR Pfam; PF00560; LRR_6.
 DR Pfam; PF01463; LRCT; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00370; LRR; 4.
 DR SMART; SM00369; LRR_typ; 6.
 KW Hypothetical protein.
 SO SEQUENCE 510 AA; 56496 MW; FF52698C2F9119E8 CRC64;

Query Match 7.6%; Score 93.5; DB 6; Length 510;
 Best Local Similarity 23.9%; Pred. No. 0.43; Mismatches 105; Indels 77; Gaps 14;
 Matches 68; Conservative 34;

QY 9 SPSSLLILLLLSPCLRGTPD-----CYFSHSPISSNFKVKFRELTDHL- 53
 DB 50 STULSLLEFNLALLSLRNGIEDVQEDALDGLTMLTLLLEHNQISS-----SLTDHTE 103
 QY 54 --LKDYPTVAVN-----LQDE--KHCALMSLEFLAQRWIEOL--KTVAGSKMOTL--LE 100
 DB 104 SKLHSIQVLYVLSNNALRTLRGSMFRNTGRLTRQLDGNQITNLIDSFGCTNLHSLRLD 163
 QY 101 DVTEIHFPTSCFPPFLPECLRFVOTN-----ISHLKD-----TCQQL 140
 DB 164 LSNMFISTYIGKDAFRPLPQ--LQEVDSLRRRLAHMPDVTEPLKQLHLHLIDKNQNSCTCDL 222
 QY 141 ----ALKPCIGKACONFSRCLEVOCCPDSSTLLPPRSPIALEATELPEPRROLLL- 193
 DB 223 HPLARFLRVYKISSAHTLNAKDLNCPSTAVAAQSVLRISFTNCPKAPNFTLVKLD 282
 QY 194 -LLLP-----LTIYLLAAMGL-----RMQARRRGELH 222
 DB 283 RSPLLPGQVALLTVLGFAGAVGLTCLGLVNMKLLQOKANEH 326

RESULT 11
 Q9ASP5 PRELIMINARY; PRT; 909 AA.
 AC O9ASP5;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Disease resistance protein RPS2.
 OS Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-2131631; PubMed-11333251;
 RA Banerjee D., Zhang X., Bent A.F.;
 RT "The leucine-rich repeat domain can determine effective interaction
 between Rps2 and other host factors in Arabidopsis RPS2-mediated
 disease resistance.";
 RT Genetics 158:439-450(2001).
 RL EMBL; AF368301; AAK38117.1; -
 DR InterPro: IPR003593; AAA_Atpase.
 DR InterPro: IPR000767; Disease_resist.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR003592; LRR_out.
 DR InterPro: IPR002182; NB-ARC.
 DR Pfam; PF00560; LRR; 4.
 DR Pfam; PF00931; NB-ARC; 1.
 DR PRINTS; PR00364; DISEASERSIST.
 DR SMART; SM00382; AAA; 1.
 DR SMART; SM00370; LRR; 4.
 KW ATP-binding.
 SO SEQUENCE 909 AA; 104613 MW; F83E0F881B409DFA CRC64;

Query Match 7.4%; Score 90.5; DB 10; Length 909;
 Best Local Similarity 22.8%; Pred. No. 1.7;
 Matches 55; Conservative 38; Mismatches 91; Indels 57; Gaps 11;

QY 14 LLLILLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTD-----HLKQDPVYVA----- 62
 DB 535 LTTLMQONSYSYKIPTEGFMHPVLRVLDLSTFSTIEIPISIVLYELVHLSGCTKIS 594
 QY 63 -----VNLQDEKHCALMSLEFL-----AQRWIEOLKTV-----AGSKMOTLLEDVNT 104
 DB 595 VLPQELGNRKRLKHLDLQRTQELQIPRDAICWLSKLEVLNLYSVAGWGLQSPQDEVE 654
 QY 105 EIHF-----VTSCTFPPLECLRF--VQNIHSLKDOTCTQLLALK-PCIGK 148
 DB 655 ELGFADLEYLEMTLGLTIVLSLETLTLEFGALHKHIQHLHVEECNDLLYFNLPSLVN 714
 QY 149 ACONFSRCLEVOCCPDSSTLLPPRSPIALEATELPEPRROLLLILLPLTVLLAAM 208
 DB 715 HGRNLR -LSISCHDLELV---TPADFENDLPS---LEVTLHSHLNTRV-----W 762
 QY 209 G 209
 DB 763 G 763

RESULT 12
 Q83443 PRELIMINARY; PRT; 326 AA.
 AC Q83443;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE VP7.
 OS Murine rotavirus.
 OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
 OX NCBI_TaxID=28527;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-EC;
 RX MEDLINE=94330134; PubMed=8053149;
 RA Dunn S.J., Burns J.W., Cross T.L., Vo P.T., Ward R.L., Bremont M.,
 RA Greenberg H.B.;
 RT "Comparison of VP4 and VP7 of five murine rotavirus strains.";
 RL Virology 203:250-259(1994).
 RL EMBL; U08422; AAB50485.1; -
 DR InterPro: IPR001963; VP7.
 DR Pfam; PF00434; VP7; 1.
 DR ProDom: PD000191; VP7; 1.
 SO SEQUENCE 326 AA; 36990 MW; B579E98A10DCF8A6 CRC64;

Query Match 7.2%; Score 88.5; DB 12; Length 326;
 Best Local Similarity 30.0%; Pred. No. 0.84; Mismatches 24; Conservative 11; Mismatches 28; Indels 17; Gaps 2;

QY 15 LLLILLLLSPCLR-----GTPDCYFSHSPISSNFKVKFRELTDHLKDYPTVA 63
 DB 38 LVLVILLSPCIRAKQNGINLPTGSMIDTAIXANSTQSDIF-----LHSTCLLYPTPAAT 91
 QY 64 NLDKHKCALMSLEFLAQRW 83
 DB 92 EMNDNSWKDLSQLFLTKGW 111
 RESULT 13
 Q83448 PRELIMINARY; PRT; 326 AA.
 AC Q83448;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE VP7.
 OS Murine rotavirus.

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OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=28327;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL.
RX MEDLINE=94310134; PubMed=8053149;
RA Dunn S.J., Burns J.W., Cross T.L., Vo P.T., Ward R.L., Bremont M.,
RA Greenberg H.B.;
RT "Comparison of VP4 and VP7 of five murine rotavirus strains.";
RL Virology 203:250-259(1994).
DR EMBL: U08427; AAA50490.1; -.
DR InterPro: IPR001963; VP7.
DR Pfam: PF00434; VP7. 1.
DR PRODOM: PD000191; VP7. 1.
SQ SEQUENCE 326 AA; 36978 MW; D6EB736833179A53 CRC64;

Query Match 7.2%; Score 88.5; DB 12; Length 326;
Best Local Similarity 30.0%; Pred. No. 0.84;
Matches 24; Conservative 11; Mismatches 28; Indels 17; Gaps 2;

OY 15 LLLLLLSPCLR-----GTPDCYFSHSPISNFKKFKRELTDHLKDYPTVAV 63
DB 38 LVLVILSPICIAQYNGINLPITGMDYVANSSTQSETF-----LSTLCLYVPTAEAT 91
OY 64 NLDEKCKALMSFLAQRW 83
DB 92 EMDNSMKDLSQLPLTRGW 111

RESULT 14
OY 09H563 PRELIMINARY; PRT; 258 AA.
AC 09H563:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE DJ149M18.1.1 (natural killer cell p4-related gene 1 (NRp44KGI)).
GN DJ149M18.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tracey A.;
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AL138967; CAC09453.1; -.
DR InterPro: IPR003599; I9.
DR InterPro: IPR003600; I9_1like.
DR InterPro: IPR003006; I9_MHC.
DR Pfam: PF00047; I9; 1.
DR SMART: SM00409; I9; 1.
DR SMART: SM00410; I9_1like; 1.
SQ SEQUENCE 258 AA; 28430 MW; F21D9055BCA5DF0F CRC64;

Query Match 7.2%; Score 88; DB 4; Length 258;
Best Local Similarity 23.8%; Pred. No. 0.73;
Matches 62; Conservative 31; Mismatches 105; Indels 62; Gaps 14;

OY 7 AWPNSLLLLLLLSPCLRGTPDCYFSHSPISNFKKFKRELTDHLK---DYPTAVAV 63
DB 2 AWRALPLPLLLLL-----FPGSOAKSKAQV-LQSVAGCTLTVCQYPTGSL 48
OY 64 NLDEKCKALMSFLAQRWIEOLK--TVAGSKMOTILEDVNTIEHFVTS----- 111
DB 49 -YEKKGMCKEA-SALVCILVYSSKPRIMAMTSRFTIMDDPDAGFTVTMTDLREDSGH 106
OY 112 --C-TFOP-----LPECLRF-----VOTNISHLKDTCTQLAIKPCI-----GKAQ 151
DB 107 YWCRIYRPSDYSVSKSVRELVVSPASASTQTSWTPRDLVSSQCTQSCVPTAGARQAP 166
OY 152 NFRCLVEVCGQPDSSSTLLP-PRSPIALTEATELPEPRPROULLLLPLTLVLAAMGL 210

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DB 167 EESPRIYVPSQPONSTLRPPAPAIALVAV-----FCGLVAKSLVLSALLVMWL 217
OY 211 RMQRRARRGE--LHEGVPLP 228
DB 218 RNRHMOHGSRSLDHFPAQPRP 237

RESULT 15
OY 094824 PRELIMINARY; PRT; 765 AA.
AC 094824:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE KIAA0716 protein.
GN KIAA0716.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=99087487; PubMed=9872452;
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Miyajima N., Tanaka A.,
RA Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XI.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 5:277-286(1998).
DR EMBL: AB018259; BRA34436.1; -.
DR InterPro: IPR000194; ATPase_a/dcentre.
DR PROSITE: PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
SQ SEQUENCE 765 AA; 86915 MW; E1C6AF0771A959F9 CRC64;

Query Match 7.2%; Score 88; DB 4; Length 765;
Best Local Similarity 20.1%; Pred. No. 2.5;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;

OY 27 GTPDCYFSHSPISNFKKFKRELTDHLK---DYPTAVANLDEKCKALW---SLFL 79
DB 236 GVPD-----NKSFYKV-----NHIMKFRYDRPFHKGTK-DKENEFKSLWERTSLYL 282
OY 80 AQ-----RW--IDOLKTVAGSKMOT---LLEVNTEIH-FVNSC-----TFOPLEPCL 121
DB 283 VQSLPGLSRMEVEKREVENMSPLENAIEVLKNNQDLTKTLLSQCTROMQNTINPLTMCL 342
OY 122 ----- 124
DB 343 NGVIDAANGSVKYGAFVKEVILSHPEDGKRIARLRLEMLEQAQLLEFGIAVHEKFEV 402
OY 125 QTNISHLKDTCTQLAIKPCIGKACONFSRCLEVQ-----CQ-----PDS 165
DB 403 PDMRPLHKKLIYDQFFVKKSLG--IOEFSACQASFPVHPNGSPRYCRNSAPASVSPG 460
OY 166 STLLPSPRIALEA 179
DB 461 TRVLPKRSPLSYPA 474

```

Search completed: November 24, 2002, 10:11:41
 Job time : 28.7768 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 24, 2002, 10:02:26 ; Search time 31.2296 Seconds
(without alignments)
985.632 Million cell updates/sec

Title: US-09-448-378-2
Perfect score: 1223
Sequence: 1 MTVLAPAMSPNSSLLLLLL.....WQRRRRGGELHPGVLPSPHP 2311

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: A_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.*

2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*

3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*

4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*

5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.*

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22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*

23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1223	100.0	231	16	AAR67540	Mouse flt-3 ligand
2	1223	100.0	231	20	AAM67768	Murine flt-3 ligand
3	1223	100.0	231	22	AAB20186	Mouse flt-3 ligand
4	1212.5	99.1	232	16	AAR66177	Mouse M0T10/T118
5	1208.5	98.8	232	22	AAB20189	Mouse flt-3 ligand
6	1006	82.3	288	22	AAU02129	Flt-3 ligand (FL)
7	1004	82.1	189	22	AAB20182	Mouse flt-3 ligand
8	879	71.9	172	22	AAB20191	Mouse flt-3 ligand
9	879	71.9	220	22	AAB20188	Mouse flt-3 ligand
10	879	71.9	220	22	AAB20190	Mouse flt-3 ligand

11	774	63.3	294	21	AAV581204	Canine Flt-3 ligand
12	772.5	63.2	235	16	AAAB6175	Human S86/S109 Flt
13	772.5	63.2	235	22	AAAB20194	Human Flt-3 ligand
14	768.5	62.8	235	26	AAAB67541	Human Flt-3 ligand
15	768.5	62.8	235	20	AAAB67769	Human Flt-3 ligand
16	768.5	62.8	235	21	AAAB69119	Full length wild t
17	768.5	62.8	235	22	AAAB20192	Human Flt-3 ligand
18	768.5	62.8	235	23	AAAB08129	Human Flt-3 polype
19	761	62.2	291	21	AAAB58210	Feline Flt-3 ligand
20	692	56.6	212	21	AAAB69721	Human Flt-3 ligand
21	687	56.2	209	21	AAAB69724	Human Flt-3 ligand
22	686	56.1	209	19	AAAB69007	Human Flt-3 ligand
23	686	56.1	209	21	AAAB69720	Mature wild type h
24	686	56.1	209	21	AAAB69723	Human Flt-3 ligand
25	685	56.0	209	21	AAAB69725	Human Flt-3 ligand
26	682	55.8	209	21	AAAB69726	Human Flt-3 ligand
27	682	55.8	209	21	AAAB69727	Human Flt-3 ligand
28	682	55.8	209	21	AAAB69729	Human Flt-3 ligand
29	680	55.6	209	21	AAAB69722	Human Flt-3 ligand
30	679.5	55.6	209	21	AAAB58206	Canine mature Flt-
31	679	55.5	268	21	AAAB59728	Human Flt-3 ligand
32	668	54.6	276	21	AAAB58207	Canine Flt-3 ligand
33	666.5	54.5	265	21	AAAB58211	Feline mature Flt-
34	663.5	54.3	185	22	AAAB20195	Human Flt-3 ligand
35	594.5	48.6	178	22	AAAB01013	Human Flt-3 ligand
36	573.5	46.9	250	21	AAAB58208	Canine mature Flt-
37	548.5	44.8	377	19	AAAB8124	Chimeric receptor
38	545	44.6	349	19	AAAB83286	Human Flt-3 ligand
39	545	44.6	349	19	AAAB83289	Human Flt-3 ligand
40	545	44.6	349	19	AAAB78005	Flt3L-1-139/Ig2b/
41	545	44.6	323	19	AAAB78008	Trimeric Flt3L-G-C
42	542.5	44.4	334	19	AAAB83290	Human Flt-3 ligand
43	542.5	44.4	334	19	AAAB78821	G-CSF-Flt-3 ligand
44	541	44.2	101	16	AAAB67174	Flt3 ligand fragme
45	541	44.2	140	19	AAAB77911	Human Flt3 ligand

ALIGNMENTS

RESULT 1	
AA067540	
ID	AA067540 standard; protein; 231 AA.
XX	
XX	
AC	AA067540;
XX	
DT	05-AUG-1995 (first entry)
XX	
DE	Mouse flt-3 ligand.
XX	
KW	Flt-3 ligand; flt3-L; anemia; cancer; AIDS;
XX	
OS	Mus sp.
XX	
Key	Location/Qualifiers
FH	1..27
FT	/label= sig-peptide
FT	
FT	Domain
FT	
FT	Domain
FT	
FT	Domain
FT	
FT	Domain
FT	
XX	
FN	EP627487-A.
XX	
PD	07-DEC-1994.
XX	
PF	
PE	19-MAY-1994;
XX	
PR	12-MAY-1993;
PR	12-AUG-1993;
PR	25-AUG-1993;
	93US-0068394.
	93US-0106463.
	93US-0111758.

PR 03-DEC-1993; 93US-0162407.
 PR 07-MAR-1994; 94US-0209502.
 PR 11-MAY-1994; 94US-0243545.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Beckmann MP, Lyman SD;
 XX
 DR WPI: 1995-008071/02.
 DR N-PSDB: AA079076.
 XX
 PT Isolated ligands for flt3 receptors - useful for treating
 PT anemia, AIDS and various cancers
 XX
 PS Disclosure; Page 25-27; 33pp; English.
 XX
 CC cDNA encoding mouse flt3-ligand (flt3-L) was isolated from a
 CC cDNA library of T-cell line F7B-0.3A4 in CV-1/EBNA-1 cells
 CC using a slide autoradiography method. Flt3-L stimulates
 CC production of progenitor and stem cells, and can be used e.g.
 CC in gene therapy protocols.
 XX
 SQ Sequence 231 AA;

Query Match 100.0%; Score 1223; DB 16; Length 231;
 Best Local Similarity 100.0%; Pred. No. 5.2e-115;
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTVLAPAMSPNSLLLLLSPLCRGTGTPDCYFSPISSEFKYKRELTDHLKDYPT 60
 |||||||
 Db 1 MTVLAPAMSPNSLLLLLSPLCRGTGTPDCYFSPISSEFKYKRELTDHLKDYPT 60
 |||||||
 OY 61 VAVNIQDEKHKALMSLEFLAQRWIEQLKTAVAGSKMOTLLEDVNTLHFVTSCTFOPLPEC 120
 |||||||
 Db 61 VAVNIQDEKHKALMSLEFLAQRWIEQLKTAVAGSKMOTLLEDVNTLHFVTSCTFOPLPEC 120
 |||||||
 OY 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDSSSTLLPPRSPIALEAT 180
 |||||||
 Db 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDSSSTLLPPRSPIALEAT 180
 |||||||
 OY 181 ELPEPRRQQLLLLLLPLTLVLLAAWGLRMQARRRGELHPGVLPSPHP 231
 |||||||
 Db 181 ELPEPRRQQLLLLLLPLTLVLLAAWGLRMQARRRGELHPGVLPSPHP 231
 |||||||

RESULT 2

AAW67768
 ID AAW67768 standard; Protein; 231 AA.

XX
 AC AAW67768;

DT 25-MAR-1999 (first entry)
 XX
 DE Murine flt3-ligand.

XX Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L;
 KW immunogenic; autoimmune disease; organ transplantation; food allergy;
 KM tissue transplantation.
 XX
 OS Mus sp.

XX
 PN MO9857655-A1.

XX
 PD 23-DEC-1998.

XX
 PF 12-JUN-1998; 98MO-US12085.

XX
 PR 17-JUN-1997; 97US-0877421.

XX
 PA (IMMV) IMMUNEX CORP.

XX
 PI Abbott MW, Mowat AM, Viney JL;

XX

DR WPI: 1999-070422/06.
 DR N-PSDB: AAW81505.

PT Methods for initiating or enhancing antigen specific immune
 PT tolerance - by using murine or human flt3 ligand
 XX
 PS Claim 1; Page 12; 25pp; English.

CC A method has been developed of initiating or enhancing: (i) an antigen-
 CC specific immune tolerance; or (ii) immunotolerance of a therapeutic
 CC immunogenic molecule by addition of a polypeptide, before, after or with
 CC the mucosal administration of an immunotolerising amount of the antigen
 CC or therapeutic molecule, respectively. The polypeptide is capable of
 CC binding the flt3 receptor and is: a) amino acids 28-x of murine flt3
 CC ligand (flt3-L), where x is an amino acid between 163-231; b) amino
 CC acids 28-y of human flt3-L, where y is an amino acid between 160-235;
 CC and c) a polypeptide that has at least 90% identity to the polypeptides
 CC of either (a) or (b). The method ameliorates the effects of autoimmune
 CC diseases, food allergies or organ or tissue rejection following
 CC transplantation. Administration of flt3-L allows lower doses of antigens
 CC to be used in vivo for mucosally administered antigens. The present
 CC sequence represents murine flt3-L.
 XX

SQ Sequence 231 AA;
 Query Match 100.0%; Score 1223; DB 20; Length 231;
 Best Local Similarity 100.0%; Pred. No. 5.2e-115;
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTVLAPAMSPNSLLLLLSPLCRGTGTPDCYFSPISSEFKYKRELTDHLKDYPT 60
 |||||||
 Db 1 MTVLAPAMSPNSLLLLLSPLCRGTGTPDCYFSPISSEFKYKRELTDHLKDYPT 60
 |||||||
 OY 61 VAVNIQDEKHKALMSLEFLAQRWIEQLKTAVAGSKMOTLLEDVNTLHFVTSCTFOPLPEC 120
 |||||||
 Db 61 VAVNIQDEKHKALMSLEFLAQRWIEQLKTAVAGSKMOTLLEDVNTLHFVTSCTFOPLPEC 120
 |||||||
 OY 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDSSSTLLPPRSPIALEAT 180
 |||||||
 Db 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDSSSTLLPPRSPIALEAT 180
 |||||||
 OY 181 ELPEPRRQQLLLLLLPLTLVLLAAWGLRMQARRRGELHPGVLPSPHP 231
 |||||||
 Db 181 ELPEPRRQQLLLLLLPLTLVLLAAWGLRMQARRRGELHPGVLPSPHP 231
 |||||||

RESULT 3

AAW20186
 ID AAW20186 standard; Protein; 231 AA.

XX
 AC AAW20186;

DT 14-MAY-2001 (first entry)
 XX

DE Mouse Flt-3 ligand.

XX Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
 KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;
 KM lymphoma; autoimmune disease; infection; gene therapy.
 XX
 OS Mus musculus.

XX
 OS Mus musculus.

XX
 FH Key Location/Qualifiers

FT Peptide 1..27 /label= Signal_peptide

FT Protein 28..231 /label= Mature_protein

FT Domain 28..188 /label= Extracellular_domain

FT Domain 189..211 /label= Transmembrane_domain

FT Domain 212..231 /label= Cytoplasmic_domain

Db 181 ELPEPRQLLLLLLLPLTLVLLAAAWGLRMQARRRGELHGVPLPSHP 232

RESULT 5
AAB20189
ID AAB20189 standard; Protein: 232 AA.
XX
AC AAB20189;
XX
XX 14-MAY-2001 (first entry)
XX
XX Mouse Flt-3 ligand.
XX
XX
XX Flt-3 ligand; fms-like tyrosine kinase; mouse; vaccine;
KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;
KW lymphoma; autoimmune disease; infection; gene therapy.
XX
XX Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..27
FT /label= Signal_peptide
FT Protein 28..232
FT /label= Mature_protein
FT Domain 28..188
FT /label= Extracellular_domain
FT Domain 189..212
FT /label= Transmembrane_domain
FT Domain 213..232
FT /label= Cytoplasmic_domain
XX
XX NO200109303-A2.
XX
XX 08-FEB-2001.
XX
XX 31-JUL-2000; 2000MO-US20679.
XX
XX 30-JUL-1999; 99US-0146170.
XX
XX (VICA-) VICAL INC.
XX
XX Hermanson CG;
XX
XX WPI: 2001-123319/13.
XX
XX N-PSDB; AAF30307.
XX
XX Immunogenic compositions comprising Flt-3 ligand encoding
PT polynucleotide and one or more antigen, or cytokine encoding
PT polynucleotides, useful for suppressing tumour growth and for treating
PT autoimmune diseases (e.g. rheumatoid arthritis) -
XX
XX
PS Claim 2; Page 125-126; 149pp; English.
XX
XX The present sequence is that of mouse fms-like tyrosine kinase
CC (Flt-3 ligand). The invention is directed to enhancing the
CC immune response of a vertebrate to an antigen or a cytokine by
CC administering in vivo, into a tissue of a vertebrate, a Flt-3
CC ligand-encoding polynucleotide, and 1 or more antigen- or
CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
CC polynucleotide may encode the present sequence or the mature
CC polypeptide. The polynucleotides are incorporated into
CC the cells of the vertebrate in vivo, and a prophylactically or
CC therapeutically effective amount of Flt-3 ligand and 1 or more
CC antigens or cytokines is produced in vivo. Pharmaceutical
CC compositions comprising the polynucleotides are useful for
CC suppressing tumour growth in a mammal. The tumour is melanoma,
CC glioma or lymphoma, particularly B-cell lymphoma. They can also
CC be used for the prophylactic and/or therapeutic treatment of:
CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
CC and C in humans), parasitic (e.g. malaria) and fungal infections;
CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
CC Various other examples of these diseases are given in the

CC specification.
XX
XX Sequence 232 AA:
Query Match 98.8%; Score 1208.5; DB 22; Length 232;
Best Local Similarity 99.1%; Pred. No. 1.5e-113;
Matches 230; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 MTVLAPAWSPNSLLLLLSPLCRGTPDCYFSHSPISSNFKVAFRELTHLKDIPVT 60
Db 1 MTVLAPAWSPNSLLLLLSPLCRGTPDCYFSHSPISSNFKVAFRELTHLKDIPVT 60
QY 61 VAVNLQDEHKCKALMSLFLAQRWIEQLKTVAGSKKQTLLEVDNPFHFVTSCTOPPEEC 120
Db 61 VAVNLQDEHKCKALMSLFLAQRWIEQLKTVAGSKKQTLLEVDNPFHFVTSCTOPPEEC 120
QY 121 LRFVOTNISHLLKDFCTQLLALKPCIGACQNFSCLEVOQCPDPSSTLLPPRSPLALEAT 180
Db 121 LRFVOTNISHLLKDFCTQLLALKPCIGACQNFSCLEVOQCPDPSSTLLPPRSPLALEAT 180
QY 181 ELPEPRPQ-ILLLLLPLTLVLLAAAWGLRMQARRRGELHGVPLPSHP 231
Db 181 ELPEPRPQ-ILLLLLPLTLVLLAAAWGLRMQARRRGELHGVPLPSHP 232
RESULT 6
AAU02129
ID AAU02129 standard; Protein: 288 AA.
XX
XX AAU02129;
XX
XX 29-AUG-2001 (first entry)
XX
XX
DE Flt-3 ligand (FL) used to make chimeric immunogenic polypeptide.
XX
XX Mouse; granulocyte-macrophage-colony stimulating factor; GM-CSF;
KW chimeric; heat shock protein; HSP; Flt-3 ligand; FL; exotoxin A;
KW ERA dif; antigenic; immunogenic; cytotoxic T cell response; tumour;
KW vaccine; immunotherapy.
XX
XX OS Unidentified.
XX
XX W0200129233-A2.
XX
XX 26-APR-2001.
XX
XX 20-OCT-2000; 2000MO-US41422.
XX
XX 20-OCT-1999; 99US-0421608.
XX
XX 09-FEB-2000; 2000US-0501097.
XX
XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
XX Wu T, Hung C;
XX
XX WPI: 2001-290921/30.
XX
XX New chimeric polypeptide, useful as anti-tumour vaccines, comprises
PT carboxy terminal fragment of heat shock protein, Flt-3 ligand or
PT cytoplasmic translocation domain of Pseudomonas exotoxin A and
PT antigenic polypeptide -
XX
XX
PS Claim 9; Fig 19; 110pp; English.
XX
XX The sequence represents the amino acid sequence of Flt-3 ligand (FL)
CC used in construction of a chimeric polypeptide comprising: (a) a first
CC polypeptide domain containing a carboxy terminal fragment of a heat shock
CC protein (HSP), an Flt-3 ligand (FL), a cytoplasmic translocation domain
CC of a Pseudomonas exotoxin A (ETA dif), or a granulocyte-macrophage colony
CC stimulating factor (GM-CSF); and (b) a second polypeptide domain
CC containing an antigenic polypeptide. A composition comprising the
CC chimeric polypeptide is useful for inducing an immune response such as a
CC cytotoxic T cell response. The nucleic acid or vector encoding the

CC chimeric polypeptide present in the composition is administered as naked
 CC DNA by gene gun or equivalent, or by liposomal formulation. These are
 CC thus useful for vaccinating a mammal against infection by inducing an
 CC immune response to a pathogen. Preferably they are useful for vaccinating
 CC a mammal against a tumour antigen. The compositions and methods are
 CC useful for stimulating or enhancing the immunogenicity of a selected
 CC antigen or stimulating or enhancing a cellular immune response specific
 CC for that antigen. The chimeric nucleic acid molecules and vaccination
 CC methods, yield potent antigen-specific immunotherapy. The polynucleotides
 CC and DNA vaccines can induce a cellular immune response that is at least
 CC 40 fold more potent than conventional DNA vaccines. The vaccines are safe
 CC and useful for administration to domesticated or agricultural animals, as
 CC well as humans, and have low immunogenicity.

CC Sequence 288 AA:

Query Match 82.3%; Score 1006; DB 22; Length 288;
 Best Local Similarity 99.5%; Pred. No. 5.3e-93;
 Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSHSPISSENFVKFRELTDHLKDYPT 60
 Db 1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSHSPISSENFVKFRELTDHLKDYPT 60
 QY 61 VAVNLQDERKCKALMSLEFLAQRWIEQLKTVAGSKMQTLLEDVNTETIHFTVSCFQPLPEC 120
 Db 61 VAVNLQDERKCKALMSLEFLAQRWIEQLKTVAGSKMQTLLEDVNTETIHFTVSCFQPLPEC 120
 QY 121 LRFVQTNISHLKDTQQLALAKPCIGKACONFSRCLEVOCCQDSSSTLLPPRSPIALEAT 180
 Db 121 LRFVQTNISHLKDTQQLALAKPCIGKACONFSRCLEVOCCQDSSSTLLPPRSPIALEAT 180
 QY 181 ELPEPRPRQL 190
 Db 181 ELPEPRPRQL 190

RESULT 7
 AAB20187
 ID AAB20187 standard; Protein: 189 AA.

AC AAB20187;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Mouse Flt-3 ligand (secreted form).
 XX
 KW Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
 KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;
 KW lymphoma; autoimmune disease; infection; gene therapy.
 XX
 OS Mus musculus.

XX
 FH Key Location/Qualifiers
 FT Peptide 1..27
 FT Protein /label= signal_peptide
 FT 28..189
 FT /label= Mature_protein
 XX

PN WO200109303-A2.
 XX
 PD 08-FEB-2001.
 XX
 PF 31-JUL-2000; 2000WO-US20679.
 XX
 PR 30-JUL-1999; 99US-0146170.
 XX
 PA (VICA-) VICAL INC.
 XX
 PI Hermanson GG;
 XX
 DR WPI: 2001-12319/13.
 DR N-PSDB: AAF30305, AAF30313.

XX Immunogenic compositions comprising Flt-3 ligand encoding
 PT polynucleotide and one or more antigen, or cytokine encoding
 PT polynucleotides, useful for suppressing tumour growth and for treating
 PT autoimmune diseases (e.g. rheumatoid arthritis) -
 XX
 PS Claim 2; Page 121; 149pp; English.

XX
 CC The present sequence is that of a secreted form of mouse Fms-like
 CC tyrosine kinase (Flt-3 ligand), lacking the transmembrane and
 CC cytoplasmic domains of the full-length form (see AAB20186). This
 CC secreted form of the Flt-3 ligand is expressed by vector VR6200
 CC (see AAF30313). The invention is directed to enhancing the
 CC immune response of a vertebrate to an antigen or a cytokine by
 CC administering in vivo, into a tissue of a vertebrate, a Flt-3
 CC ligand-encoding polynucleotide, such as VR6200, and 1 or more
 CC antigen- or cytokine-encoding polynucleotides. The polynucleotides
 CC are incorporated into the cells of the vertebrate in vivo, and a
 CC prophylactically or therapeutically effective amount of Flt-3
 CC ligand and 1 or more antigens or cytokines is produced in vivo.
 CC Pharmaceutical compositions comprising the polynucleotides are
 CC useful for suppressing tumour growth in a mammal. The tumour is
 CC melanoma, glioma or lymphoma, particularly B-cell lymphoma. The
 CC co-injection of VR6200 and tumour-specific antigen-encoding plasmid
 CC VR1623 into mice significantly enhanced protection from tumour
 CC challenge. The claimed pharmaceutical compositions can also be
 CC used for the prophylactic and/or therapeutic treatment of:
 CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
 CC and C in humans), parasitic (e.g. malaria) and fungal infections;
 CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
 CC osteoarthritis); (c) cancer; and (d) Anjeszky's disease in pigs.
 CC Various other examples of these diseases are given in the
 CC specification.

CC Sequence 189 AA:

Query Match 82.1%; Score 1004; DB 22; Length 189;
 Best Local Similarity 100.0%; Pred. No. 4.8e-93;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSHSPISSENFVKFRELTDHLKDYPT 60
 Db 1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSHSPISSENFVKFRELTDHLKDYPT 60
 QY 61 VAVNLQDERKCKALMSLEFLAQRWIEQLKTVAGSKMQTLLEDVNTETIHFTVSCFQPLPEC 120
 Db 61 VAVNLQDERKCKALMSLEFLAQRWIEQLKTVAGSKMQTLLEDVNTETIHFTVSCFQPLPEC 120
 QY 121 LRFVQTNISHLKDTQQLALAKPCIGKACONFSRCLEVOCCQDSSSTLLPPRSPIALEAT 180
 Db 121 LRFVQTNISHLKDTQQLALAKPCIGKACONFSRCLEVOCCQDSSSTLLPPRSPIALEAT 180
 QY 181 ELPEPRPRQL 189
 Db 181 ELPEPRPRQL 189

RESULT 8
 AAB20191
 ID AAB20191 standard; Protein: 172 AA.

XX
 AC AAB20191;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Mouse Flt-3 ligand.

XX
 KW Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
 KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;
 KW lymphoma; autoimmune disease; infection; gene therapy.
 XX
 OS Mus musculus.

Key	Location/Qualifiers
FT	Peptide 1..27
FT	Protein /label= Signal_peptide 28..172
FT	Protein /label= Mature_protein
XX	MO200109303-A2.
XX	08-FEB-2001.
XX	31-JUL-2000; 2000WO-US20679.
XX	30-JUL-1999; 99US-0146170.
XX	(VICA-) VICAL INC.
XX	Hermanson GG;
XX	WPI; 2001-123319/13.
XX	N-PSDB; AAF30309.
XX	Immunogenic compositions comprising Flt-3 ligand encoding polynucleotides and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. rheumatoid arthritis) -
XX	Claim 2; Page 130; 149pp; English.
XX	The present sequence is that of mouse Fms-like tyrosine kinase (Flt-3 ligand). The invention is directed to enhancing the immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a Flt-3 ligand-encoding polynucleotide, and 1 or more antigen- or cytokine-encoding polynucleotides. The Flt-3 ligand-encoding polynucleotide may encode the present sequence or the mature polypeptide. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of Flt-3 ligand and 1 or more antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, glioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of: (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B and C in humans), parasitic (e.g. malaria) and fungal infections; (b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs. Various other examples of these diseases are given in the specification.
XX	SO Sequence 172 AA:
XX	Query Match 71.9%; Score 879; DB 22; Length 172;
XX	Best Local Similarity 98.2%; Pred. No. 1.7e-80;
XX	Matches 165; Conservative 1; Mismatches 2; Indels 0; Gaps 0.
QY	1 MVLPAWSPNSLLLSLSPCLKGPDPQCYSHSPISNFKVKKPRELTDHLKDPVT 60
DB	1 MVLPAWSPNSLLLSLSPCLKGPDPQCYSHSPISNFKVKKPRELTDHLKDPVT 60
QY	61 VAVNLDEKCKALMSLFLAQRNIEQLKTVAGSKMOTLEDVNTETHEVYTSCTFOPLPKC 120
DB	61 VAVNLDEKCKALMSLFLAQRNIEQLKTVAGSKMOTLEDVNTETHEVYTSCTFOPLPKC 120
QY	121 LRFVQTNISHLKDTCTQLALKPCIGKACONSRLCEVOCOPDSSSTL 168
DB	121 LRFVQTNISHLKDTCTQLALKPCIGKACONSRLCEVOCOPDSSSTL 168

RESULT 9

AAB20185

ID AAB20188 standard; Protein; 220 AA.

XX

AC	AAB20188;
XX	
DT	14-MAY-2001 (first entry)
XX	
DE	Mouse Flt-3 ligand.
XX	
KW	Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine; immunotherapy; therapy; tumour; cancer; melanoma; glioma; lymphoma; autoimmune disease; infection; gene therapy.
XX	
OS	Mus musculus.
XX	
EH	Key Location/Qualifiers
FT	Peptide 1..27
FT	/Label= Signal_peptide
FT	Protein 28..220
FT	/label= Mature_protein
XX	
PN	WO200109303-A2.
XX	
PD	08-FEB-2001.
XX	
PX	31-JUL-2000; 2000WO-US20679.
PX	
PR	30-JUL-1999; 99US-0146170.
XX	
PA	(VICA-) VICAL INC.
PI	Hermanson GG;
DR	WPI: 2001-123319/13.
DR	N-PsDB: AAF30306.
XX	
PT	Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. rheumatoid arthritis) -
PS	Claim 2; Page 123-124; 149pp; English.
XX	
CC	The present sequence is that of mouse fms-like tyrosine kinase (Flt-3 ligand). The invention is directed to enhancing the immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a Flt-3 ligand-encoding polynucleotide, and 1 or more antigen- or cytokine-encoding polynucleotides. The Flt-3 ligand-encoding polynucleotide may encode the present sequence or the mature polypeptide. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of Flt-3 ligand and 1 or more antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, glioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of: (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B and C in humans), parasitic (e.g. malaria) and fungal infections; (b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Anjeszky's disease in pigs. Various other examples of these diseases are given in the specification.
SQ	Sequence 220 AA:
XX	
Query Match	71.9%; Score 879; DB 22; Length 220;
Best local Similarity	82.3%; Pred. No. 2,4e-80;
Matches 177; Conservative	5; Mismatches 21; Indels 12; Gaps
OY	1 MTVALPAPMSNSSLLILLILSLPCLAGTTPCCYRSHSPISSEFVKKRELTDHLIKOYPVT 60
D8	1 MTVALPAPMSNSSLLILLILSLPCLAGTTPCCYRSHSPISSEFVKKRELTDHLIKOYPVT 60
OY	61 VAVNIODEKRCALMISFLAQRWIEQLTVAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120

CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense
 CC oligonucleotides). The proteins may be used to raise antibodies and to
 CC screen for modulators of activity, while the antibodies may be used in
 CC detection, and in drug targeting.

XX Sequence 294 AA;

Query Match 63.3%; Score 774; DB 21; Length 294;
 Best Local Similarity 70.2%; Pred. No. 1.3e-69;
 Matches 158; Conservative 23; Mismatches 38; Indels 6; Gaps 4;

QY 1 MTVLAPAMSPNSLSLLLSLSPCLRGTPDCYFSHPISSENEKVKFRELTDHLKDPYPT 60
 1 MTVLAPAMSPNS-LLLSLSPCLRGTPDCYFSHPISSENEKVKFRELTDHLKDPYPT 59
 DB 61 VAVNIODEKHKALMSFLAQRWIEOLKTVAGSKMOTLLEDVNTETHEFTVTSCTFQPLPEC 120
 60 VASNIODEDELCAFWRLVLAQRWVRLQAVAGSQMQLLEAVNTEHFVTECAFOPLPSC 119
 QY 121 LRFVQTNISHLKDKTCTQLLAKPCIGACQNFSCLEVOCCOPDSSSTLLPPRSPIALEAT 180
 120 LRFVQTNISHLQDTSQDLALAKPWITR--RNFSCLELQCOOPDSSSTLLPPRSPIALEAT 177
 DB 181 ELPEPR-PROQLLLLLPLTVLLAAMGLRMQARRRRELHPG 224
 178 ALPAPOAPR--LLLLLLPVALLLMSTAMCLHMRRRRRRRSPYPG 220

RESULT 12

ID AAR66175 standard; Peptide: 235 AA.

XX AAR66175;
 AC AAR66175;
 XX 10-AUG-1995 (first entry)
 DT Human s86/S109 Flt3 ligand peptide sequence.
 XX Human s86/S109 Flt3 ligand peptide sequence.
 DE Flt3 ligand; tyrosine kinase receptor ligand.
 KM Flt3 ligand; tyrosine kinase receptor ligand.
 XX Homo sapiens.
 OS Homo sapiens.
 XX MO9426891-A.
 PN 24-NOV-1994.
 PD 18-MAY-1994; 94MO-US05150.
 XX 19-MAY-1993; 93US-0065231.
 PR 07-JUL-1993; 93US-0089263.
 PR 16-JUL-1993; 93US-0092549.
 PR 13-AUG-1993; 93US-0106340.
 PR 24-AUG-1993; 93US-0112391.
 PR 19-NOV-1993; 93US-015111.
 PR 03-DEC-1993; 93US-0162413.
 XX (INRM) INST NAT SANTE & RECH MEDICALE.
 PA (SCHE) SCHERING CORP.
 XX Birnbaum D, Culpepper JA, Hannum CH, Lee FD;
 PI WPI: 1995-006787/01.
 XX N-PSDB: AAG79642.
 DR New ligand for the Flt3 tyrosine kinase receptor - and related
 XX nucleic acid, vectors, host cells and antibodies, useful for
 PT

PT treating abnormal cell physiology and proliferation, e.g. cancer,
 PT also for diagnosis and drug screening
 XX Claim 11; Page 76-77; 90pp; English.

XX A cDNA library from the human stromal cell line 293SV48, in
 CC pMT8, was screened with an 800 bp fragment derived from
 CC mouse clone T118. This fragment encompasses the coding region
 CC conserved between two mouse clones, T118 and T110. Approx. 20
 CC positive clones were selected and partially sequenced. Two
 CC clones, S86 and S109, were found to be approx. 75% homologous
 CC to the mouse clones over the first 163 AAs. Clone S86 continued
 CC to show homology to T110 until the stop codon, although to a
 CC lesser degree, for an overall homology of 66%. Clones T118 and
 CC S109 do not show homology to each other or to the other clones
 CC after mouse residue 163 (human residue 160). An additional mouse
 CC clone designated M88 has a 29 AA insert at the junction between
 CC the common and divergent portions of the mouse ligand.

XX Sequence 235 AA;

Query Match 63.2%; Score 772.5; DB 16; Length 235;
 Best Local Similarity 70.7%; Pred. No. 1.4e-69;
 Matches 164; Conservative 17; Mismatches 42; Indels 9; Gaps 4;

QY 1 MTVLAPAMSPNSLSLLLSLSPCLRGTPDCYFSHPISSENEKVKFRELTDHLKDPYPT 60
 1 MTVLAPAMSP--TLYULLLLLSLSTGTCDFSHSPISSENEKVKFRELTDHLKDPYPT 59
 DB 61 VAVNIODEKHKALMSFLAQRWIEOLKTVAGSKMOTLLEDVNTETHEFTVTSCTFQPLPEC 120
 60 VASNIODEDELCAFWRLVLAQRWVRLQAVAGSQMQLLEAVNTEHFVTECAFOPLPSC 119
 QY 121 LRFVQTNISHLKDKTCTQLLAKPCIGACQNFSCLEVOCCOPDSSSTLLPPRSPIALEAT 180
 120 LRFVQTNISRLQDSQDLALAKPWITR--QNFSCLELQCOOPDSSSTLLPPRSPIALEAT 177
 DB 181 ELPEPR-PROQLLLLLPLTVLLAAMGLRMQARRR---GELHGVPLP 228
 178 APTAPQPP--LLLLLLPVALLLMSTAMCLHMRRRRRRRSPYPG 227

RESULT 13

ID AAB20194 standard; Protein: 235 AA.

XX AAB20194;
 AC AAB20194;
 XX 14-MAY-2001 (first entry)
 DT Human Flt-3 ligand.
 XX Human Flt-3 ligand.
 DE Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;
 XX immunotherapy; therapy; tumour; cancer; melanoma; glioma;
 KM lymphoma; autoimmune disease; infection; gene therapy.
 XX Homo sapiens.
 OS Homo sapiens.
 XX Key
 FH Peptide
 FT 1..26
 FT /label= Signal_peptide
 FT 27..235
 FT /label= Mature_protein
 FT Domain
 FT 27..182
 FT /label= Extracellular_domain
 FT 183..205
 FT /label= Transmembrane_domain
 FT 206..235
 FT /label= Cytoplasmic_domain
 XX WO200109303-A2.
 XX 08-FEB-2001.
 XX

PF	31-JUL-2000; 2000MO-US20679.
XX	
FR	30-JUL-1999; 99US-0146170.
XX	
PA	(VICAL-) VICAL INC.
XX	
PI	Hermanson GG;
XX	
DR	WPI: 2001-123319/13.
XX	N-PSDB; AAF30312.
PT	Immunogenic compositions comprising Flt-3 ligand encoding
PT	polynucleotide and one or more antigen, or cytokine encoding
PT	polynucleotides, useful for suppressing tumour growth and for treating
XX	autoimmune diseases (e.g. rheumatoid arthritis) -
XX	
XX	Claim 2; Page 137-138; 149pp; English.
XX	
CC	The present sequence is that of human Fms-like tyrosine kinase
CC	(Flt-3 ligand). The invention is directed to enhancing the
CC	immune response of a vertebrate to an antigen or a cytokine by
CC	administering in vivo, into a tissue of a vertebrate, a Flt-3
CC	ligand-encoding polynucleotide, and 1 or more antigen- or
CC	cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
CC	polynucleotide may encode the present full-length human Flt-3
CC	ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235
CC	of the Flt-3 ligand. The polynucleotides are incorporated into
CC	the cells of the vertebrate in vivo, and a prophylactically or
CC	therapeutically effective amount of Flt-3 ligand and 1 or more
CC	antigens or cytokines is produced in vivo. Pharmaceutical
CC	compositions comprising the polynucleotides are useful for
CC	suppressing tumour growth in a mammal. The tumour is melanoma,
CC	glioma or lymphoma, particularly B-cell lymphoma. They can also
CC	be used for the prophylactic and/or therapeutic treatment of:
CC	(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
CC	and C in humans), parasitic (e.g. malaria) and fungal infections;
CC	(b) autoimmune diseases (e.g. rheumatoid arthritis and
CC	osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
CC	Various other examples of these diseases are given in the
CC	specification.
XX	
XX	Sequence 235 AA:
SO	
Query Match	63.2%; Score 772.5; DB 22; Length 235;
Best Local Similarity	70.7%; Pred. No. 1.4e-69;
Matches 164; Conservative 17; Mismatches 42; Indels 9; Gaps	
OY	1 MTVLAPAMSNSSLILLLLSFCLGPPDCCYFSSPISNFKFRLMDHLKQDVPV 60
	IIIIIIII :: IIIIIII :: IIIIIII :: IIIIIII :: IIIIIII :: IIIIIII ::
Db	1 MTLVAPAMSP-TTYIIIIIIIISSGLSGYDCDFQHSPISSDFAKIKELSYLIQDYPV 59
OY	61 VAVVUODEKCKAKLMSIFLAORWIEQDKTVAGSKMQLLEDVNTIEIHFVYSCFQPLPEC 120
	IIIIII :: IIIIIII :: IIIIIII :: IIIIIII :: IIIIIII :: IIIIIII ::
Db	60 VASVUODEEELCGALIMRWIVLAORMERLKVAVAGSKMGGLELVENIEIHFVYKCAFOPPSC 119
OY	121 LRFQVNTINSHLKDCTQTLALPKPCIGKAKCONFESRCLFVQCOPOSSSTLLPSPRIAEAT 180
	IIIIII :: IIIIIII :: IIIIIII :: IIIIIII :: IIIIIII :: IIIIIII ::
Db	120 LRFQVNTINSHLQETSEQVALKLPWTR--QNFSGLELQCOPOSSSTLLPSPMSRPLEAT 177
OY	181 ELPEPRRQLLLLLPLPLTVILVLAAMGLNMQARRR---GELHPEGVLP 228
	IIIIII :: IIIIIII :: IIIIIII :: IIIIIII :: IIIIIII :: IIIIIII ::
Db	178 APVAPDP--LLIIIIILPVGLIIILAAAMCLAMQIQRRTPRPGGVPPSP 227
RESULT 14	
AAR67541	
ID	AAR67541 standard; Protein; 235 AA.
XX	
AC	AAR67541;
XX	
DT	05-AUG-1995 (first entry)
XX	

DE	Human flt-3 ligand.
XX	
KW	Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy.
XX	
OS	Homo sapiens.
XX	
FT	Key Location/Qualifiers
FT	Peptide 1..26
FT	/label= Sig-peptide
FT	/note= "signal peptide may extend to position 27"
FT	Domain 27..182
FT	/label= Extracellular_domain
FT	/note= "extracellular domain may start at position 28"
FT	Domain 183..205
FT	/label= Transmembrane_domain
FT	Domain 206..235
FT	/label= Cytoplasmic_domain
XX	
PN	EPE27487-A.
XX	
PD	07-DEC-1994.
XX	
PF	19-MAY-1994; 94EP-0303575.
PR	24-MAY-1993; 93US-0068394.
PR	12-AUG-1993; 93US-0106463.
PR	25-AUG-1993; 93US-0111758.
PR	03-DEC-1993; 93US-0162407.
PR	07-MAR-1994; 94US-0209502.
PR	11-MAY-1994; 94US-0243545.
XX	
PA	(IMMV) IMMUNEX CORP.
XX	
FI	Beckmann MP, Lyman SD;
XX	
DR	WPI: 1995-008071/02.
DR	N-PDB: AAO79079.
XX	
PT	Isolated ligands for flt 3 receptors - useful for treating
PT	anaemia, AIDS and various cancers
XX	
PS	Disclosure; Page 29-30; 33pp; English.
CC	A human T-cell lambda-gtl0 random primed cDNA library was
CC	screened with a fragment corresponding to the extracellular
CC	domain of mouse flt3 ligand (flt3-L) (nt 103-516 of AAO79076)
CC	to isolate human flt3-L cDNA. Flt-3 stimulates progenitor and
CC	stem cells, and can be used e.g. in gene therapy protocols.
XX	
SQ	Sequence 235 AA:
Query Match	62.8%; Score 768.5; DB 16; Length 235;
Best Local Similarity	70.3%; Pred. No. 3.6e-69;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps	
OY	1 MTVALPAPMNSSTLTLTLLSPRCRGTPDCEFSHSPISNFKKPRELTDHLKDPYT 60
Dd	1 MTVALPAMSP-TTYLLLTLLSSGLSGTODCSFQHSPPSSFAKKRELSDYLDQYPVT 59
OY	61 VAVNLDEKHCKAKLSFLAQRWIEOLKTVAAGKMOTILEDVNTETHFVTSCTFOPLPEC 120
Dd	60 VASNIODEELCGGLMRVLIAORMERLKTVAAASKMOGILLERVNTEIHFVTKCAFOPPPC 119
OY	121 LRFQQTINSHLKDTCQTLALAKPGICGAQNFCSCLEVCOCOPSSTLPPRSPIAEAT 180
Dd	120 LRFQQTINSHLDETSEQVALKPWTTR--QNFSCLELCQCPPOSSSLPPRPMGRPLEAT 177
OY	181 ELPEPRROQLLLLLLPGLTVLLVLAAGLMQARRRR---GELHPGVLP 228
Dd	178 APTAPQP--TLTLILPVGLLIILAAACMLHWQRTTRRTPRRGQVPVPSP 227

RESULT 15

AAW67769 standard: Protein: 235 AA.

ID AAW67769;

AC AAW67769;

DT 25-MAR-1999 (first entry)

DE Human flt3-ligand.

KW Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L;

KW Immunogenic; autoimmune disease; organ transplantation; food allergy;

KW tissue transplantation.

OS Homo sapiens.

PN W09857655-A1.

PD 23-DEC-1998.

PF 12-JUN-1998; 98WO-US12085.

PR 17-JUN-1997; 97US-0877421.

PA (IMMV) IMMUNEX CORP.

PI Abbott NM, Mowat AM, Viney JL;

DR WPI: 1999-070422/06.

PS N-PSDB; AAW61506.

PT Methods for initiating or enhancing antigen specific immune

PT tolerance - by using murine or human flt3 ligand

PS Claim 1; Page 14-15; 25pp; English.

XX A method has been developed of initiating or enhancing: (i) an antigen-

CC specific immune tolerance; or (ii) immunotolerance of a therapeutic

CC immunogenic molecule by addition of a polypeptide, before, after or with

CC the mucosal administration of an immunotolerising amount of the antigen

CC or therapeutic molecule, respectively. The polypeptide is capable of

CC binding the flt3 receptor and is: a) amino acids 28-x of murine flt3

CC ligand (flt3-L), where x is an amino acid between 163-231; b) amino

CC acids 28-y of human flt3-L, where y is an amino acid between 160-235;

CC and c) a polypeptide that has at least 90% identity to the polypeptides

CC of either (a) or (b). The method ameliorates the effects of autoimmune

CC diseases, food allergies or organ or tissue rejection following

CC transplantation. Administration of flt3-L allows lower doses of antigens

CC to be used in vivo for mucosally administered antigens. The present

CC sequence represents human flt3-L.

SQ Sequence 235 AA;

Query Match 62.8%; Score 768.5; DB 20; Length 235;
Best Local Similarity 70.3%; Pred. No. 3.6e-69;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

OY 1 MTVLAPAMSPNSLLILLILLLSPCLRGTPDCYFSHSPISSNFKKFRRLDHLKDDYPT 60
| | | | | : | | | | | | | | | | | | | | | : | | | | |
DB 1 MTVLAPAMSP-TTYLLILLILLLSSGLSTGQDSFQHSPISSDFAVKIRELSDYLDYPT 59
| | | | | : | | | | | | | | | | | | | | | : | | | | |
OY 61 VAVNIÖDERKCKALMSLFLAORWIEOLTKVAGSKMÖTLLEDVNTIEHFVTSCTFOPLPEC 120
| | | | | : | | | | | | | | | | | | | | | : | | | | |
DB 60 VASNIÖDERKCGLMRLVLAORWMLKTVAGSKMÖGLLEEVNTEIHFVTKCAFOPEPSC 119
| | | | | : | | | | | | | | | | | | | | | : | | | | |
OY 121 LRFVQTNISHLKDTCTÖLLAIKPCIGKACQNFSCLEVCQCPDSSTLLPPRSPIALEAT 180
| | | | | : | | | | | | | | | | | | | | | : | | | | |
DB 120 LRFVQTNISRLQETSEQLVALKPWITR--QNFSCRLELQCPDSTLLPPWSPRPLEAT 177
| | | | | : | | | | | | | | | | | | | | | : | | | | |
OY 181 ELPEPPRÖLLILLPLTLVLVLAAGLMORARRR---GELHPCVPLP 228
| : | | | | | : | | | | | | | | | | | | | | | : | | | | |
DB 178 APTAPQPP--LTLILLPLVGLLLAAACMLWÖRTRRTPRREGQVPPVPSF 227
| : | | | | | : | | | | | | | | | | | | | | | : | | | | |

Search completed: November 24, 2002, 10:10:13
Job time : 32.2296 secs

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OM protein - protein search, using sw model

Run on: November 24, 2002, 10:11:46 ; Search time 8.42704 Seconds

(without alignments)
429,309 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223

Sequence: 1 MTVALPAPMSPNSLLLLLLL.....WQRRRRGELHPGVLPDPSHP 231

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/PCYUS_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	1223	100.0	231	9	US-10-095-449-2
2	1223	100.0	231	10	US-09-448-378-2
3	1223	100.0	231	10	US-09-983-806-2
4	768.5	62.8	235	9	US-10-095-449-6
5	768.5	62.8	235	10	US-09-448-378-1
6	768.5	62.8	235	10	US-09-983-806-6
7	768.5	62.8	235	10	US-09-904-536-1
8	724.5	59.2	137	10	US-09-904-536-19
9	692	56.6	212	10	US-09-904-536-10
10	687	56.1	209	10	US-09-904-536-15
11	686	56.1	209	10	US-09-904-536-14
12	685	56.1	209	10	US-09-904-536-16
13	685	56.0	209	10	US-09-904-536-16
14	682	55.8	209	10	US-09-904-536-9
15	682	55.8	209	10	US-09-904-536-12
16	682	55.8	209	10	US-09-904-536-17
17	680	55.6	209	10	US-09-904-536-11
18	679	55.5	209	10	US-09-904-536-13
19	678	55.4	209	10	US-09-904-536-8

20	95.5	7.8	909	10	US-09-867-852-142	Sequence 142, App
21	94	7.7	355	10	US-09-948-018-2	Sequence 2, App11
22	92	7.5	885	10	US-09-867-852-2	Sequence 2, App11
23	89.5	7.3	874	10	US-09-826-508-26	Sequence 26, App1
24	89.5	7.3	941	9	US-09-793-139-47	Sequence 47, App1
25	89.5	7.3	941	10	US-09-818-879-47	Sequence 47, App1
26	89.5	7.3	941	10	US-09-211-755B-47	Sequence 47, App1
27	80.5	6.6	391	10	US-09-800-729-208	Sequence 208, App
28	80.5	6.6	391	10	US-09-987-107-35	Sequence 35, App1
29	80	6.5	9	9	US-09-992-598-57	Sequence 57, App1
30	80	6.5	811	10	US-09-187-368-1	Sequence 1, App11
31	80	6.5	811	10	US-09-989-722-57	Sequence 57, App1
32	80	6.5	811	10	US-09-989-722-57	Sequence 57, App1
33	80	6.5	811	10	US-09-989-729-57	Sequence 57, App1
34	80	6.5	811	10	US-09-989-727-57	Sequence 57, App1
35	80	6.5	811	10	US-09-989-731-57	Sequence 57, App1
36	80	6.5	811	10	US-09-989-732-57	Sequence 57, App1
37	80	6.5	811	10	US-09-991-073-57	Sequence 57, App1
38	80	6.5	811	10	US-09-990-442-57	Sequence 57, App1
39	80	6.5	811	10	US-09-991-163-57	Sequence 57, App1
40	80	6.5	811	10	US-09-993-604-57	Sequence 57, App1
41	80	6.5	811	10	US-09-990-456-57	Sequence 57, App1
42	80	6.5	811	10	US-09-989-721-57	Sequence 57, App1
43	80	6.5	811	12	US-10-052-586-414	Sequence 414, App
44	79.5	6.5	365	10	US-09-867-530-2026	Sequence 2026, App
45	77.5	6.3	929	9	US-09-793-139-4	Sequence 4, App11

ALIGNMENTS

RESULT 1
US-10-095-449-2
Sequence 2, Application US/10095449

Patent No. US20020160004A1

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.

Beckmann, M. Patricia

TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Stephen L. Malaska, Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.0.1

SOFTWARE: Microsoft Word, Version #5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/095,449

FILING DATE: 13-Mar-2002

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/669,692

FILING DATE: 24-JUN-1996

APPLICATION NUMBER: 08/08/162,407

FILING DATE: December 3, 1993

APPLICATION NUMBER: 08/111,758

FILING DATE: August 25, 1993

APPLICATION NUMBER: 08/106,463

FILING DATE: August 12, 1993

APPLICATION NUMBER: 08/068,394

FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655

REFERENCE/DOCKET NUMBER: 2813-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-095-449-2

Query Match	100.0%;	Score 1223;	DB 9;	Length 231;
Best Local Similarity	100.0%;	Pred. No. 1.5e-107;		
Matches 231; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

QY	1	MTVLAPAMSPSSLLIIIIIIISPCRLGPPDCYFESHSPISNNFKKAPFELIDHLLKXVPV	60
QY	1	MTVLAPAMSPSSLLIIIIIIISPCRLGPPDCYFESHSPISNNFKKAPFELIDHLLKXVPV <td>60</td>	60
Db	1	MTVLAPAMSPSSLLIIIIIIISPCRLGPPDCYFESHSPISNNFKKAPFELIDHLLKXVPV	60
QY	61	VAVNLQDEKHCCKALMSFLAQRIWEOLKTYAGSKMQLLEDVNIENHFVSTCTFQPIREC	120
QY	61	VAVNLQDEKHCCKALMSFLAQRIWEOLKTYAGSKMQLLEDVNIENHFVSTCTFQPIREC	120
Db	61	VAVNLQDEKHCCKALMSFLAQRIWEOLKTYAGSKMQLLEDVNIENHFVSTCTFQPIREC	120
QY	121	LRFVQVNIINSHLLKTCYQVLLAKFCIGKACONFSRCLEVOVOCQDPSLLPSPRIALEAT	180
QY	121	LRFVQVNIINSHLLKTCYQVLLAKFCIGKACONFSRCLEVOVOCQDPSLLPSPRIALEAT	180
Db	121	LRFVQVNIINSHLLKTCYQVLLAKFCIGKACONFSRCLEVOVOCQDPSLLPSPRIALEAT	180
QY	181	ELPEPRPQOLLIIIIIIIPITLVIIILAAAMGLRMQARARGELHPEVPLPSHP	231
QY	181	ELPEPRPQOLLIIIIIIIPITLVIIILAAAMGLRMQARARGELHPEVPLPSHP	231
Db	181	ELPEPRPQOLLIIIIIIIPITLVIIILAAAMGLRMQARARGELHPEVPLPSHP	231

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RESULT 2
US-09-448-378-2
; Sequence 2, Application US/09448378
; Patent No. US20020034517A1
; GENERAL INFORMATION:
; APPLICANT: Brasel, Kenneth
; TITLE OF INVENTION: Dendritic Cell Stimulatory Factor
; FILE REFERENCE: 2836-D
; CURRENT APPLICATION NUMBER: US/09/448,378
; CURRENT FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Mus sp.
; US-09-448-378-2

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Query Match	100.0%;	Score 1223;	DB 10;	Length 231;
Best Local Similarity	100.0%;	Pred. No. 1.5e-107;		
Matches 231; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

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Dd	1	MTVLAPAMSPSSLLLLLLLPCLRKTPPOCYTSHSPTSSNEKKFFELDHLDKDPVT	60
QY	61	VAVNLODEKHCKALMSLFLEAQRWTEQLKYVAAGSKMQTLIDVNTVEIHFEVTSCTEOPILPEC	120
Dd	61	VAVNLODEKHCKALMSLFLEAQRWTEQLKYVAAGSMQTLLEDVNTVEIHFVTSCTFOPLPEC	120
QY	121	LREVOITMISHLKDTQTQLLAALKPCIGKACQNFSCLEYCQPDSDSTLPPRSPIALPEAT	180
Dd	121	LRFVOTIMISHLKDTQTQLLAKPCIGKACQNFSCLEYCQPDSDSTLPPRSPIALPEAT	180
QY	181	ELRPERRROLILLIIILLPILVLVLLAAAWGLRMQRRARRRGELHGCVLPJPSHP	231
Dd	181	ELRPERRROLILLIIILLPILVLVLLAAAWGLRMQRRARRRGELHGCVLPJPSHP	231

RESULT 3
US-09-983-805-2

Sequence 2, Application US/09983806
Patent No. US20020107365A1
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for Flt3/Flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/983, 806
FILING DATE: 25-Oct-2001
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/444, 626
FILING DATE: 19-MAY-1995
APPLICATION NUMBER: US 08/162, 407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111, 758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106, 463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068, 394
FILING DATE: May 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756622
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-983-806-2

Query Match	100.0%;	Score 1223;	DB 10;	Length 231;
Best Local Similarity	100.0%;	Pred. No. 1.5e-107;		
Matches 231;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MYVLAAPWSPNSLLIIIIIIISPCRLRGTPCPCYPSPHSISSNEFKVKKRELTIDHLKDYPVT	60
	1	MYVLAAPWSPNSLLIIIIIIISPCRLRGTPCPCYPSPHSISSNEFKVKKRELTIDHLKDYPVT	60
Db	1	MYVLAAPWSPNSLLIIIIIIISPCRLRGTPCPCYPSPHSISSNEFKVKKRELTIDHLKDYPVT	60
QY	61	VAVNIDDEKCKALMSLELAORMIETQLKTVAGSGSMQITLEDVNTLEHFAVTSCTPOPLPEC	120
Db	61	VAVNIDDEKCKALMSLELAORMIETQLKTVAGSGSMQITLEDVNTLEHFAVTSCTPOPLPEC	120
QY	61	VAVNIDDEKCKALMSLELAORMIETQLKTVAGSGSMQITLEDVNTLEHFAVTSCTPOPLPEC	120
Db	61	VAVNIDDEKCKALMSLELAORMIETQLKTVAGSGSMQITLEDVNTLEHFAVTSCTPOPLPEC	120
QY	121	LRFVQTNISHLIKDTCTQLLAKPCIGKACONFSRCLEVOCCQDSDSTLLPPRSPIALBAT	180
Db	121	LRFVQTNISHLIKDTCTQLLAKPCIGKACONFSRCLEVOCCQDSDSTLLPPRSPIALBAT	180
QY	121	LRFVQTNISHLIKDTCTQLLAKPCIGKACONFSRCLEVOCCQDSDSTLLPPRSPIALBAT	180
Db	121	LRFVQTNISHLIKDTCTQLLAKPCIGKACONFSRCLEVOCCQDSDSTLLPPRSPIALBAT	180
QY	181	ELPEPPRRQULLIIIIIIIEPLTVLLAAMWGLRMQARARRGSLHNGVPLPSHP	231
Db	181	ELPEPPRRQULLIIIIIIIEPLTVLLAAMWGLRMQARARRGSLHNGVPLPSHP	231
QY	181	ELPEPPRRQULLIIIIIIIEPLTVLLAAMWGLRMQARARRGSLHNGVPLPSHP	231
Db	181	ELPEPPRRQULLIIIIIIIEPLTVLLAAMWGLRMQARARRGSLHNGVPLPSHP	231

RESULT 4

US-10-095-449-6
; Sequence 6, Application US/10095449
; Patent No. US2002016004A1
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for Flt3/Flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/095,449
; FILING DATE: 13-Mar-2002
; CLASSIFICATION: 530
; PRIORITY DATA:
; APPLICATION NUMBER: 08/669,692
; FILING DATE: 24-JUN-1996
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-095-449-6

Query Match 62.8%; Score 768.5; DB 9; Length 235;
Best Local Similarity 70.3%; Pred. No. 6.5e-65;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MTVLAPAMSPSSLLILLSPCLRGPDYFSPHSPISSENFVKYKPRELDHLKDYPT 60
| | | | | : | | | | | | | | | | | | | | | : | | | | |
DB 1 MTVLAPAMSP--TYYLLILLSSLSGTSQDCSFQHSPISSDFAVKIRELSDYLDQYPT 59
| | | | | : | | | | | | | | | | | | | | | : | | | | |
QY 61 VAVNLQDEKCKALMSFLAQRWIEQLKTVAGSKMOTLLEDVNTETIHFTVTSCTFQPLPEC 120
| | | | | : | | | | | : | | | | | | | | | | | | | | | : | | | | |
DB 60 VASNLQDEELCGGLMRLVLAQRMMERLKTAVAGSKMOTLLEDVNTETIHFTVTSCTFQPLPEC 119
| | | | | : | | | | | : | | | | | | | | | | | | | | | : | | | | |
QY 121 LRFVQNTISHLKDTQYLLAKPCIGKACONFSRCLEVOCCOPDSSITLPPRSPILAEAT 180
| | | | | : | | | | | : | | | | | | | | | | | | | | | : | | | | |
DB 120 LRFVQNTISHLKDTQYLLAKPCIGKACONFSRCLEVOCCOPDSSITLPPRSPILAEAT 177
| | | | | : | | | | | : | | | | | | | | | | | | | | | : | | | | |
QY 181 ELPEPRPQQLILLPLTVLLAAAGLWRQARRR---GELHGVPLP 228
| : | | | | | : | | | | | | | | | | | | | | | : | | | | |
DB 178 APTARQPP--LLILLPLVGLLLAAAGLWQRTRRRTTRPRGQVPPVPS 227
| : | | | | | : | | | | | | | | | | | | | | | : | | | | |

RESULT 5
US-09-448-378-1
; Sequence 1, Application US/09448378
; Patent No. US20020034517A1
; GENERAL INFORMATION:
; APPLICANT: Brasel, Kenneth
; TITLE OF INVENTION: Dendritic Cell Stimulatory Factor
; FILE REFERENCE: 2836-D
; CURRENT APPLICATION NUMBER: US/09/448,378
; CURRENT FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-448-378-1

Query Match 62.8%; Score 768.5; DB 10; Length 235;
Best Local Similarity 70.3%; Pred. No. 6.5e-65;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MTVLAPAMSPSSLLILLSPCLRGPDYFSPHSPISSENFVKYKPRELDHLKDYPT 60
| | | | | : | | | | | | | | | | | | | | | : | | | | |
DB 1 MTVLAPAMSP--TYYLLILLSSLSGTSQDCSFQHSPISSDFAVKIRELSDYLDQYPT 59
| | | | | : | | | | | | | | | | | | | | | : | | | | |
QY 61 VAVNLQDEKCKALMSFLAQRWIEQLKTVAGSKMOTLLEDVNTETIHFTVTSCTFQPLPEC 120
| | | | | : | | | | | : | | | | | | | | | | | | | | | : | | | | |
DB 60 VASNLQDEELCGGLMRLVLAQRMMERLKTAVAGSKMOTLLEDVNTETIHFTVTSCTFQPLPEC 119
| | | | | : | | | | | : | | | | | | | | | | | | | | | : | | | | |
QY 121 LRFVQNTISHLKDTQYLLAKPCIGKACONFSRCLEVOCCOPDSSITLPPRSPILAEAT 180
| | | | | : | | | | | : | | | | | | | | | | | | | | | : | | | | |
DB 120 LRFVQNTISHLKDTQYLLAKPCIGKACONFSRCLEVOCCOPDSSITLPPRSPILAEAT 177
| | | | | : | | | | | : | | | | | | | | | | | | | | | : | | | | |
QY 181 ELPEPRPQQLILLPLTVLLAAAGLWRQARRR---GELHGVPLP 228
| : | | | | | : | | | | | | | | | | | | | | | : | | | | |
DB 178 APTARQPP--LLILLPLVGLLLAAAGLWQRTRRRTTRPRGQVPPVPS 227
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RESULT 6
US-09-983-806-6
; Sequence 6, Application US/09983806
; Patent No. US20020107365A1
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for Flt3/Flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/983,806
; FILING DATE: 25-Oct-2001
; CLASSIFICATION: 530
; PRIORITY DATA:
; APPLICATION NUMBER: US/08/444,626
; FILING DATE: 19-MAY-1995
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993


```

; GENERAL INFORMATION:
; APPLICANT: Gradadis, Thomas J.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-16

Query Match          56.0%; Score 685; DB 10; Length 209;
Best Local Similarity 69.8%; Pred. No. 3.8e-57;
Matches 143; Conservative 15; Mismatches 39; Indels 8; Gaps 3;

QY 28 TPDCEFSHPISNFKYKRELTDLKDYPTVAVNLQDEKHKALMSFLAQRTEQL 87
DB 1 TQDCSFQHSPISSDFAVKIRELSYDLQDYPTVASNLQDEELCGGLMRLVLAQRMMERL 60
QY 88 KTVAGSKMQTLLEVDNTEIHFTVSCFQPLPECLRFVQTNISHLKDTCTQLALKPCIG 147
DB 61 KTVAGSKMQGLLEVRNTEIHFTVKCAFPQPPSCLRFVQTNISRLQETSQVALKPWIT 120
QY 148 KACQNSRCLEVOQOPDSSSTLLPPRSPIALEATELPEPRRQLLLLLLPLTVLAAA 207
DB 121 R--QNFSCRLELOQOPDSSSTLLPPWSPRPLEATAPTAQPQP--LLLLLLLPVGLLLAAA 176
QY 208 WGLRMQARRR---GELHGPVPLP 228
DB 177 WCLHMQTRRRTPRPGQVPPVPS 201

RESULT 14
US-09-904-536-9
; Sequence 9, Application US/09904536
; Patent No. US2002011475A1
; GENERAL INFORMATION:
; APPLICANT: Gradadis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-9

Query Match          55.8%; Score 682; DB 10; Length 209;
Best Local Similarity 69.3%; Pred. No. 7.2e-57;
Matches 142; Conservative 15; Mismatches 40; Indels 8; Gaps 3;

QY 28 TPDCEFSHPISNFKYKRELTDLKDYPTVAVNLQDEKHKALMSFLAQRTEQL 87
DB 1 TQDCSFQHSPISSDFAVKIRELSYDLQDYPTVASNLQDEELCGGLMRLVLAQRMMERL 60
QY 88 KTVAGSKMQTLLEVDNTEIHFTVSCFQPLPECLRFVQTNISHLKDTCTQLALKPCIG 147
DB 61 KTVAGSKMQGLLEVRNTEIHFTVKCAFPQPPSCLRFVQTNISRLQETSQVALKPWIT 120
QY 148 KACQNSRCLEVOQOPDSSSTLLPPRSPIALEATELPEPRRQLLLLLLPLTVLAAA 207
DB 121 R--QNFSCRLELOQOPDSSSTLLPPWSPRPLEATAPTAQPQP--LLLLLLLPVGLLLAAA 176
QY 208 WGLRMQARRR---GELHGPVPLP 228
DB 177 WCLHMQTRRRTPRPGQVPPVPS 201

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DB 121 R--QNFSCRLELOQOPDSSSTLLPPWSPRPLEATAPTAQPQP--LLLLLLLPVGLLLAAA 176
QY 208 WGLRMQARRR---GELHGPVPLP 228
DB 177 WCLHMQTRRRTPRPGQVPPVPS 201

RESULT 15
US-09-904-536-12
; Sequence 12, Application US/09904536
; Patent No. US2002011475A1
; GENERAL INFORMATION:
; APPLICANT: Gradadis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-12

Query Match          55.8%; Score 682; DB 10; Length 209;
Best Local Similarity 69.3%; Pred. No. 7.2e-57;
Matches 142; Conservative 15; Mismatches 40; Indels 8; Gaps 3;

QY 28 TPDCEFSHPISNFKYKRELTDLKDYPTVAVNLQDEKHKALMSFLAQRTEQL 87
DB 1 TQDCSFQHSPISSDFAVKIRELSYDLQDYPTVASNLQDEELCGGLMRLVLAQRMMERL 60
QY 88 KTVAGSKMQTLLEVDNTEIHFTVSCFQPLPECLRFVQTNISHLKDTCTQLALKPCIG 147
DB 61 KTVAGSKMQGLLEVRNTEIHFTVKCAFPQPPSCLRFVQTNISRLQETSQVALKPWIT 120
QY 148 KACQNSRCLEVOQOPDSSSTLLPPRSPIALEATELPEPRRQLLLLLLPLTVLAAA 207
DB 121 R--QNFSCRLELOQOPDSSSTLLPPWSPRPLEATAPTAQPQP--LLLLLLLPVGLLLAAA 176
QY 208 WGLRMQARRR---GELHGPVPLP 228
DB 177 WCLHMQTRRRTPRPGQVPPVPS 201

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Job time : 9.42704 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 24, 2002, 10:10:16 ; Search time 135.328 Seconds
(without alignments)
1100.533 Million cell updates/sec

Title: US-09-448-378-2
1223
Perfect score: 1223
Sequence: 1 MVLAPAWSPNSLLILL.....WQARRRGELHPGVLPSPHP 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 64473110 residues
Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*
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6: /cgn2_6/ptodata/1/paa/US082_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US084_COMB.pep:*
9: /cgn2_6/ptodata/1/paa/US085_COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
11: /cgn2_6/ptodata/1/paa/US087_COMB.pep:*
12: /cgn2_6/ptodata/1/paa/US088_COMB.pep:*
13: /cgn2_6/ptodata/1/paa/US089_COMB.pep:*
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26: /cgn2_6/ptodata/1/paa/US102_COMB.pep:*
27: /cgn2_6/ptodata/1/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1223	100.0	231	1 PCT-US98-12085-2	Sequence 2, Appl1
2	1223	100.0	231	4 US-08-068-394-2	Sequence 2, Appl1
3	1223	100.0	231	5 US-08-106-463-2	Sequence 2, Appl1
4	1223	100.0	231	5 US-08-111-758-2	Sequence 2, Appl1
5	1223	100.0	231	5 US-08-162-407-2	Sequence 2, Appl1
6	1223	100.0	231	8 US-08-444-625-2	Sequence 2, Appl1

7	1223	100.0	231	8 US-08-444-626-2	Sequence 2, Appl1
8	1223	100.0	231	8 US-08-444-632-2	Sequence 2, Appl1
9	1223	100.0	231	10 US-08-669-692-2	Sequence 2, Appl1
10	1223	100.0	231	12 US-08-877-421-2	Sequence 2, Appl1
11	1223	100.0	231	18 US-09-448-378-2	Sequence 2, Appl1
12	1223	100.0	231	20 US-09-629-430B-8	Sequence 8, Appl1
13	1223	100.0	231	20 US-09-983-806-2	Sequence 8, Appl1
14	1223	100.0	231	23 US-10-095-449-2	Sequence 2, Appl1
15	1223	100.0	231	24 US-10-095-449-2	Sequence 2, Appl1
16	1212.5	99.1	232	27 US-60-368-263-2	Sequence 38, Appl1
17	1212.5	99.1	232	5 US-08-155-111-38	Sequence 38, Appl1
18	1212.5	99.1	232	5 US-08-162-413-38	Sequence 38, Appl1
19	1212.5	99.1	232	6 US-08-261-553-38	Sequence 38, Appl1
20	1212.5	99.1	232	8 US-08-472-168-38	Sequence 38, Appl1
21	1212.5	99.1	232	8 US-08-484-882-38	Sequence 38, Appl1
22	1212.5	99.1	232	8 US-08-486-661-38	Sequence 38, Appl1
23	1212.5	99.1	232	21 US-09-791-537-86787	Sequence 86787, A
24	1212.5	99.1	232	21 US-09-629-430B-13	Sequence 13, Appl1
25	1208.5	98.8	232	20 US-09-629-430B-9	Sequence 9, Appl1
26	1208.5	98.8	232	21 US-09-791-537-51625	Sequence 51625, A
27	1208.5	98.8	232	19 US-09-501-097-25	Sequence 25, Appl1
28	1208.5	98.8	232	19 US-09-501-097A-25	Sequence 25, Appl1
29	1004	82.1	189	1 PCT-US02-08033-18	Sequence 18, Appl1
30	1004	82.1	189	20 US-09-629-430B-9	Sequence 9, Appl1
31	879	71.9	172	1 PCT-US02-08033-20	Sequence 20, Appl1
32	879	71.9	172	20 US-09-629-430B-17	Sequence 17, Appl1
33	879	71.9	220	21 US-09-791-537-18574	Sequence 18574, A
34	874	71.5	220	20 US-09-629-430B-11	Sequence 11, Appl1
35	774	63.3	169	20 US-09-629-430B-15	Sequence 15, Appl1
36	774	63.3	294	17 US-09-322-409-7	Sequence 17, Appl1
37	774	63.3	294	18 US-09-451-527-7	Sequence 7, Appl1
38	774	63.3	294	18 US-10-218-654-7	Sequence 7, Appl1
39	772.5	63.2	235	26 US-10-262-439-7	Sequence 7, Appl1
40	772.5	63.2	235	5 US-08-155-111-34	Sequence 34, Appl1
41	772.5	63.2	235	5 US-08-162-413-34	Sequence 34, Appl1
42	772.5	63.2	235	6 US-08-261-553-34	Sequence 34, Appl1
43	772.5	63.2	235	8 US-08-472-168-34	Sequence 34, Appl1
44	772.5	63.2	235	8 US-08-484-882-34	Sequence 34, Appl1
45	772.5	63.2	235	8 US-08-486-661-34	Sequence 34, Appl1
			20	US-09-629-430B-23	Sequence 23, Appl1

ALIGNMENTS

RESULT 1
PCT-US98-12085-2
Sequence 2, Application PC/US9812085
GENERAL INFORMATION:
APPLICANT: IMMUNEX CORPORATION
TITLE OF INVENTION: A Method of Enhancing Antigen-Specific Peripheral Immune To
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM/PC Compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, Version 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/12085
FILING DATE: 12-JUN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2855-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US98-12085-2

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Best Local Similarity 100.0%; Pred. No. 3.5e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 LRFVQTNISHLKDTCTQLLALPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPIALEAT 180
Db 121 LRFVQTNISHLKDTCTQLLALPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQQLLLLLPLTVLLAAAGLRWQARRRGEIHPGVLPSPH 231
Db 181 ELPEPRRQQLLLLLPLTVLLAAAGLRWQARRRGEIHPGVLPSPH 231

RESULT 2
US-08-068-394-2
Sequence 2, Application US/08068394
GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,394
FILING DATE: 19930524
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-068-394-2

Query Match 100.0%; Score 1223; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.5e-110;

Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 VAVNLQDEKCKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTETHEVTSCTFQPLPEC 120
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Db 121 LRFVQTNISHLKDTCTQLLALPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPIALEAT 180
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Db 181 ELPEPRRQQLLLLLPLTVLLAAAGLRWQARRRGEIHPGVLPSPH 231

RESULT 3
US-08-106-463-2
Sequence 2, Application US/08106463
GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/106,463
FILING DATE: 19930812
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-106-463-2

Query Match 100.0%; Score 1223; DB 5; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.5e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLKDYPT 60
QY 61 VAVNLQDEKCKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTETHEVTSCTFQPLPEC 120
Db 61 VAVNLQDEKCKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTETHEVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLLALPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPIALEAT 180
Db 121 LRFVQTNISHLKDTCTQLLALPCIGKACQNFSCLEVOCCOPDSSSTLLPPRSPIALEAT 180

Db 121 LRFVQTNISHLKDKTCQTOLALPCIGKACQNSRCLLEVQCPDSSSTLLPPRSPIALEAT 180
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Db 181 ELPEPRRQLLLLLLPLTLVLLAAAGLRWQRRARRGELHPGVLPSPH 231

RESULT 4

US-08-111-758-2
; Sequence 2, Application US/08111758
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/111,758
; FILING DATE: August 25, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-111-758-2

Query Match 100.0%; Score 1223; DB 5; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.5e-110; Indels 0; Gaps 0;
Matches 231; Conservative 0; Mismatches 0;

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QY 121 LRFVQTNISHLKDKTCQTOLALPCIGKACQNSRCLLEVQCPDSSSTLLPPRSPIALEAT 180
Db 121 LRFVQTNISHLKDKTCQTOLALPCIGKACQNSRCLLEVQCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQLLLLLLPLTLVLLAAAGLRWQRRARRGELHPGVLPSPH 231
Db 181 ELPEPRRQLLLLLLPLTLVLLAAAGLRWQRRARRGELHPGVLPSPH 231

RESULT 5

US-08-162-407-2
; Sequence 2, Application US/08162407
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-162-407-2

Query Match 100.0%; Score 1223; DB 5; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.5e-110; Indels 0; Gaps 0;
Matches 231; Conservative 0; Mismatches 0;

QY 1 MTVLAPAMSPNSLLLLLSPLCRGTPDCYFSHSPISSENFVKFRELTDHLKDYPT 60
Db 1 MTVLAPAMSPNSLLLLLSPLCRGTPDCYFSHSPISSENFVKFRELTDHLKDYPT 60
QY 61 VAVNLQDEKHCALMSLFLAQRWIEQLKTVAAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120
Db 61 VAVNLQDEKHCALMSLFLAQRWIEQLKTVAAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDKTCQTOLALPCIGKACQNSRCLLEVQCPDSSSTLLPPRSPIALEAT 180
Db 121 LRFVQTNISHLKDKTCQTOLALPCIGKACQNSRCLLEVQCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQLLLLLLPLTLVLLAAAGLRWQRRARRGELHPGVLPSPH 231
Db 181 ELPEPRRQLLLLLLPLTLVLLAAAGLRWQRRARRGELHPGVLPSPH 231

RESULT 6

US-08-444-625-2

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; Sequence 2, Application US/08444625
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,625
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-444-625-2

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Best Local Similarity 100.0%; Pred. No. 3.5e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MTVLAPAMSPNSLSLILLLSPCLRGTPDCYFSHPISSNFKVRFRELTDLKLDYPT 60
QY 61 VAVNLQDEKHKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTLHFVTSCTFQPLPEC 120
DB 61 VAVNLQDEKHKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTLHFVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDTQTQLALKPCIGKACQNFSCRLEVOQCPDSSSTLLPPRSPIALEAT 180
DB 121 LRFVQTNISHLKDTQTQLALKPCIGKACQNFSCRLEVOQCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQULLLLPLTLVLLAAAGLRLWQARRRREGELHPGVPLPSHP 231
DB 181 ELPEPRRQULLLLPLTLVLLAAAGLRLWQARRRREGELHPGVPLPSHP 231

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RESULT 7

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US-08-444-626-2
; Sequence 2, Application US/08444626
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,626
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-444-626-2

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Query Match          100.0%; Score 1223; DB 8; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.5e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVLAPAMSPNSLSLILLLSPCLRGTPDCYFSHPISSNFKVRFRELTDLKLDYPT 60
DB 1 MTVLAPAMSPNSLSLILLLSPCLRGTPDCYFSHPISSNFKVRFRELTDLKLDYPT 60
QY 61 VAVNLQDEKHKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTLHFVTSCTFQPLPEC 120
DB 61 VAVNLQDEKHKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTLHFVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDTQTQLALKPCIGKACQNFSCRLEVOQCPDSSSTLLPPRSPIALEAT 180
DB 121 LRFVQTNISHLKDTQTQLALKPCIGKACQNFSCRLEVOQCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQULLLLPLTLVLLAAAGLRLWQARRRREGELHPGVPLPSHP 231
DB 181 ELPEPRRQULLLLPLTLVLLAAAGLRLWQARRRREGELHPGVPLPSHP 231

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RESULT 8
US-08-444-632-2
; Sequence 2, Application US/08444632
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,632
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-444-632-2

Query Match 100.0%; Score 1223; DB 8; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.5e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
RESULT 9
US-08-669-692-2
; Sequence 2, Application US/08669692
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,692
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-669-692-2

Query Match 100.0%; Score 1223; DB 10; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.5e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 10
US-08-877-421-2
; Sequence 2, Application US/08877421
; GENERAL INFORMATION:
; APPLICANT: Viney, Joanne L.
; APPLICANT: Mowatt, Allan McI.
; APPLICANT: Abbott, Nicholas
; TITLE OF INVENTION: A Method of Enhancing Antigen-Specific Peripheral Immune Tol
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Macintosh 7.6
; SOFTWARE: Microsoft Word, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,421
; FILING DATE: 17-JUN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2855
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; MOLECULE TYPE: protein
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-877-421-2
Query Match 100.0%; Score 1223; DB 12; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.5e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPNSLLILLILSPCLRGTPDCYFSHSPISSNKVKFRELTHLKDYPVT 60
D 1 MTVALPAMSPNSLLILLILSPCLRGTPDCYFSHSPISSNKVKFRELTHLKDYPVT 60
QY 61 VAVNLDEKHCCKALMSLFLAQRWIEOLKTVAGSKMOTILEDVNTLHFVTSCTFQPLPEC 120
D 61 VAVNLDEKHCCKALMSLFLAQRWIEOLKTVAGSKMOTILEDVNTLHFVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLALPKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPIALEAT 180
D 121 LRFVQTNISHLKDTCTQLALPKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQLLLLLLLLPLTLVLLAAWGLRMQRRARRGELHPGVLPDPSHP 231
D 181 ELPEPRRQLLLLLLLLPLTLVLLAAWGLRMQRRARRGELHPGVLPDPSHP 231

RESULT 11
US-09-448-378-2
; Sequence 2, Application US/09448378
; GENERAL INFORMATION:
; APPLICANT: Brasel, Kenneth
; TITLE OF INVENTION: Dendritic Cell Stimulatory Factor
; FILE REFERENCE: 2836-D
; CURRENT APPLICATION NUMBER: US/09/448,378
; CURRENT FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 2
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-448-378-2
Query Match 100.0%; Score 1223; DB 18; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.5e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPNSLLILLILSPCLRGTPDCYFSHSPISSNKVKFRELTHLKDYPVT 60
D 1 MTVALPAMSPNSLLILLILSPCLRGTPDCYFSHSPISSNKVKFRELTHLKDYPVT 60
QY 61 VAVNLDEKHCCKALMSLFLAQRWIEOLKTVAGSKMOTILEDVNTLHFVTSCTFQPLPEC 120
D 61 VAVNLDEKHCCKALMSLFLAQRWIEOLKTVAGSKMOTILEDVNTLHFVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLALPKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPIALEAT 180
D 121 LRFVQTNISHLKDTCTQLALPKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQLLLLLLLLPLTLVLLAAWGLRMQRRARRGELHPGVLPDPSHP 231
D 181 ELPEPRRQLLLLLLLLPLTLVLLAAWGLRMQRRARRGELHPGVLPDPSHP 231

RESULT 12
US-09-629-430B-8
; Sequence 8, Application US/09629430B
; GENERAL INFORMATION:
; APPLICANT: Hermanson, Gary George
; TITLE OF INVENTION: FLT-3-Ligand-Encoding Polynucleotide as a
; FILE REFERENCE: 1530.0130001
; CURRENT APPLICATION NUMBER: US/09/629,430B
; CURRENT FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 60/146,170
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-629-430B-8
Query Match 100.0%; Score 1223; DB 20; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.5e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPNSLLILLILSPCLRGTPDCYFSHSPISSNKVKFRELTHLKDYPVT 60
D 1 MTVALPAMSPNSLLILLILSPCLRGTPDCYFSHSPISSNKVKFRELTHLKDYPVT 60
QY 61 VAVNLDEKHCCKALMSLFLAQRWIEOLKTVAGSKMOTILEDVNTLHFVTSCTFQPLPEC 120
D 61 VAVNLDEKHCCKALMSLFLAQRWIEOLKTVAGSKMOTILEDVNTLHFVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLALPKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPIALEAT 180
D 121 LRFVQTNISHLKDTCTQLALPKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQLLLLLLLLPLTLVLLAAWGLRMQRRARRGELHPGVLPDPSHP 231
D 181 ELPEPRRQLLLLLLLLPLTLVLLAAWGLRMQRRARRGELHPGVLPDPSHP 231

RESULT 13
US-09-983-806-2
; Sequence 2, Application US/09983806
; GENERAL INFORMATION:
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```

;
; APPLICANT: Lyman, Stewart D.
; Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/983,806
; FILING DATE: 25-Oct-2001
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,626
; FILING DATE: 19-MAY-1995
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-983-806-2

Query Match 100.0%; Score 1223; DB 23; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.5e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPNSLLLLLLSPCLRGTPDCYFSHSPISNFKYKRELTDLKDYPT 60
DB 1 MTVALPAMSPNSLLLLLLSPCLRGTPDCYFSHSPISNFKYKRELTDLKDYPT 60
QY 61 VAVNIODEKHCKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTETIHFVTSCTFOPLPEC 120
DB 61 VAVNIODEKHCKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTETIHFVTSCTFOPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPALAEAT 180
DB 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPALAEAT 180
QY 181 ELPEPRRQLLLLLLPLTLVLAAAGLIRWQRRARRGELHFGVPLPSHP 231
DB 181 ELPEPRRQLLLLLLPLTLVLAAAGLIRWQRRARRGELHFGVPLPSHP 231

RESULT 14
US-10-095-449-2
; Sequence 2, Application US/10095449
; GENERAL INFORMATION:
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;
; APPLICANT: Lyman, Stewart D.
; Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/095,449
; FILING DATE: 13-Mar-2002
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/669,692
; FILING DATE: 24-JUN-1996
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-095-449-2

Query Match 100.0%; Score 1223; DB 24; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.5e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPNSLLLLLLSPCLRGTPDCYFSHSPISNFKYKRELTDLKDYPT 60
DB 1 MTVALPAMSPNSLLLLLLSPCLRGTPDCYFSHSPISNFKYKRELTDLKDYPT 60
QY 61 VAVNIODEKHCKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTETIHFVTSCTFOPLPEC 120
DB 61 VAVNIODEKHCKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTETIHFVTSCTFOPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPALAEAT 180
DB 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNSRCLEVOCCOPDSSSTLLPPRSPALAEAT 180
QY 181 ELPEPRRQLLLLLLPLTLVLAAAGLIRWQRRARRGELHFGVPLPSHP 231
DB 181 ELPEPRRQLLLLLLPLTLVLAAAGLIRWQRRARRGELHFGVPLPSHP 231

RESULT 15
US-60-368-263-2
; Sequence 2, Application US/60368263
; GENERAL INFORMATION:
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; APPLICANT: McKenna, Hilary J.
; APPLICANT: Liebowitz, David N.
; APPLICANT: Maliszewski, Charles R.
; TITLE OF INVENTION: METHODS OF USING FLT-3 LIGAND IN IMMUNIZATION PROTOCOLS
; FILE REFERENCE: 3399
; CURRENT APPLICATION NUMBER: US/60/368,263
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Mus sp
; US-60-368-263-2

Query Match 100.0%; Score 1223; DB 27; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.5e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVLAPAMSPNSLLLLLLLSPLRSTPCYFSHSPISSNFKVYKPRELTDHLTKDYPT 60
DB 1 MTVLAPAMSPNSLLLLLLLSPLRSTPCYFSHSPISSNFKVYKPRELTDHLTKDYPT 60
QY 61 VAVNLDEKCKALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTETIHFTVSTCFQPLPEC 120
DB 61 VAVNLDEKCKALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTETIHFTVSTCFQPLPEC 120
QY 121 LRFVOTNISHLMDTCTQLALKPCIGKACONFSRCLEVOCCOPDSTLLPPRSPIALEAT 180
DB 121 LRFVOTNISHLMDTCTQLALKPCIGKACONFSRCLEVOCCOPDSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQQLLLLLLPLTVLVLAAMGLRQARRRGELHPCVPLPSHP 231
DB 181 ELPEPRRQQLLLLLLPLTVLVLAAMGLRQARRRGELHPCVPLPSHP 231

Search completed: November 24, 2002, 10:17:26
Job time: 136.328 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 24, 2002, 10:08:46 ; Search time 14.6245 Seconds
(without alignments)
1544.781 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242
Sequence: 1 MTVLAPAWSPTTYLLLLLL.....RPGEOVPVPSQDILLVEH 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	235	2 I38440	flt3 ligand - huma
2	864.5	69.6	245	2 S43293	FLT3/FLK2 ligand (
3	834	67.1	178	2 I39076	flt3 ligand altern
4	768.5	61.9	231	2 A49265	flt3/flk-2 ligand
5	606.5	48.8	220	2 S43291	FLT3/FLK2 ligand (
6	606.5	48.8	220	2 I58343	flt3 ligand isofor
7	93	7.5	1217	2 T22672	hypothetical prote
8	92	7.4	661	1 TNBE12	74k alpha trans-in
9	89.5	7.2	474	2 T19543	hypothetical prote
10	89	7.2	387	2 I48201	adhalin - golden h
11	89	7.2	793	2 S60735	splicing factor SF
12	88.5	7.1	238	2 AB1990	hypothetical prote
13	88.5	7.1	1386	2 T00257	hypothetical prote
14	88	7.1	753	2 J00532	OP protein - kenne
15	87.5	7.0	919	1 A32290	protein-tyrosine-p
16	87	7.0	910	2 A53137	tyrosine kinase re
17	86.5	7.0	590	2 A40437	glutamic acid-rich
18	86	6.9	299	2 T17832	hypothetical prote
19	86	6.9	485	2 A33647	sulfated surface p
20	86	6.9	746	2 T28004	hypothetical prote
21	85	6.8	289	2 A87646	hypothetical prote
22	85	6.8	366	2 A37374	Fe gamma (196) rec
23	84	6.8	263	2 T03162	tegment protein 6
24	84	6.8	757	2 A39283	gamma-glutamyl car
25	83.5	6.7	199	2 E75630	hypothetical prote
26	83.5	6.7	530	2 A45690	transactivator EBN
27	83	6.7	1509	2 T19486	hypothetical prote
28	82.5	6.6	418	2 T19800	hypothetical prote
29	82.5	6.6	426	2 I36948	Ig epsilon-chain -

30	82.5	6.6	512	2 D40829	activin receptor 1
31	82.5	6.6	513	2 J01484	proline/leucine-r1
32	82	6.6	106	2 T06479	hypothetical prote
33	82	6.6	854	2 T23837	hypothetical prote
34	81.5	6.6	485	2 C75460	stromelysin 3 (EC
35	81.5	6.6	488	2 S13423	hypothetical prote
36	81.5	6.6	958	2 T13593	related to cytoske
37	81.5	6.6	1119	2 T50995	cysteine-rich exte
38	81	6.5	196	2 B48232	hypothetical prote
39	81	6.5	209	2 A48232	probable transpos
40	81	6.5	294	2 A12016	Ig epsilon chain C
41	81	6.5	388	2 S15591	class I cytochrome
42	81	6.5	428	1 BHHU	hypothetical prote
43	80.5	6.5	636	2 JH0047	hypothetical prote
44	80.5	6.5	1176	2 T49482	hypothetical prote
45	80.5	6.5	1306	2 T13592	hypothetical prote

ALIGNMENTS

RESULT 1					
I38440					
flt3 ligand - human					
C:Species: Homo sapiens (man)					
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000					
C:Accession: I38440; I39075; S43292					
R:Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S.S.; Downe					
Blood 83, 2795-2801, 1994					
A:Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor fo					
A:Reference number: I38440; MUID:94235842; PMID:8180375					
A:Accession: I38440					
A:Status: preliminary; translated from GB/EMBL/DBJ					
A:Molecule type: mRNA					
A:Residues: 1-235 <RES>					
A:Cross-references: EMBL:003858; NID:g494978; PIDN:AAA19825.1; PID:g494979					
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.					
Oncogene 11, 1165-1172, 1995					
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.					
A:Reference number: I39075; MUID:96032581; PMID:7565977					
A:Accession: I39075					
A:Status: preliminary; translated from GB/EMBL/DBJ					
A:Molecule type: DNA					
A:Residues: 1-235 <RES>					
A:Cross-references: EMBL:029874; NID:g1072036; PIDN:AAA90949.1; PID:g1072037					
R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.;					
felt, A.; Muench, M.; Kelner, G.; Namiakawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik					
Nature 368, 643-648, 1994					
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoie					
A:Reference number: S43290; MUID:94195428; PMID:8145851					
A:Accession: S43292					
A:Status: preliminary					
A:Molecule type: mRNA					
A:Residues: 1-71, 'A', '73-235 <HAN>					
A:Cross-references: GB:U04806; NID:g483844; PIDN:AAA17999.1; PID:g483845					
A:Note: the authors translated the codon AGT for residue 25 as Met					
C:Genetics:					
A:Introns: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3					
Query Match					
Best Local Similarity 100.0%; Pred. No. 5.4e-95; Length 235;					
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
OY	1	MTVLAPAWSPTTYLLLLLSGLSTGQCSPFHSPFISSDFAVKIRELSDYLLQDPYTV	60		
DB	1	MTVLAPAWSPTTYLLLLLSGLSTGQCSPFHSPFISSDFAVKIRELSDYLLQDPYTV	60		
OY	61	ASNLQDEELCGIWRVLVAQRWMERLKTVAAGSKMGLERVTETHFVTKCAFQPPPSCL	120		
DB	61	ASNLQDEELCGIWRVLVAQRWMERLKTVAAGSKMGLERVTETHFVTKCAFQPPPSCL	120		
OY	121	RFVQNTNIRLQETSQVIAKRWITRONFNSCLELQCPDSSSTLPPPSPPLEATAPT	180		
DB	121	RFVQNTNIRLQETSQVIAKRWITRONFNSCLELQCPDSSSTLPPPSPPLEATAPT	180		

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Db      121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLLELOCCQDPDSTLLPPWSPRPLEATAP 180
QY      181 APOPLLLELLLPVGLLLAAAMCLHMQRTRRTPRGEQVPPVPSQDILLVNH 235
      181 APOPLLLELLLPVGLLLAAAMCLHMQRTRRTPRGEQVPPVPSQDILLVNH 235

RESULT 2
FLTK2 ligand (clone S109) - human
C:Species: Homo sapiens (man)
C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S43293
R:Hanum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; K&
felt, A.; Muench, M.; Keilner, G.; Nankawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A
Nature 368, 643-648, 1994
A:Title: Ligand for FLTK2 receptor tyrosine kinase regulates growth of haematopoietic
A:Reference number: S43290; MUID:94195428; PMID:8145851
A:Accession: S43293
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-245 <HAN>
A:Note: the authors translated the codon AGG for residue 25 as Met

Query Match      69.68; Score 864.5; DB 2; Length 245;
Best Local Similarity 73.08; Pred. No. 1.2e-66;
Matches 176; Conservative 7; Mismatches 27; Indels 31; Gaps 3;

QY      1 MTVALPAMSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVY 60
Db      1 MTVALPAMSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVY 60
QY      61 ASNLQDEELCGGLWRLVLAQRMMERLKTVAAGSKMGLLEVRNTEIHFTVKCAFQPPSC 120
Db      61 ASNLQDEELCGALWRLVLAQRMMERLKTVAAGSKMGLLEVRNTEIHFTVKCAFQPPSC 120
QY      121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLLELOCCQDPDSTLLPPWSPRPLEATAP 180
Db      121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLLELOCCQDPDSTLLPPWSPRPLEATAP 177
QY      181 APOPL-----PLLELLLPVGLLLAAAMCLHMQRTRRTPRGEQVPPVPS 227
      181 APOPL-----PLLELLLPVGLLLAAAMCLHMQRTRRTPRGEQVPPVPS 227
Db      178 WPRPHRPEDEAHRGESP-----ARGLIAMTQKRLARGSLPWAFLPSP 222
QY      228 Q 228
      228 Q 228
Db      223 E 223

RESULT 3
FLTK2 ligand alternatively spliced isoform - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: I39076
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.
Oncogene 11, 1165-1172, 1995
A:Title: Structural analysis of human and murine fltk3 ligand genomic loci.
A:Reference number: I39075; MUID:96032581; PMID:7566977
A:Accession: I39076
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-178 <RES>
A:Cross-references: EMBL:U29874; NID:g1072036; PIDN:AAA90950.1; PID:g1072038
C:Genetics:
A:introns: 11/3; 48/3; 66/3; 114/3; 161/1

Query Match      67.18; Score 834; DB 2; Length 178;
Best Local Similarity 100.08; Pred. No. 3.3e-64;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTVALPAMSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVY 60
      1 MTVALPAMSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVY 60

Db      121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLLELOCCQDPDSTLLPPWSPRPLEATAP 180
QY      121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLLELOCCQDPDSTLLPPWSPRPLEATAP 160
      121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLLELOCCQDPDSTLLPPWSPRPLEATAP 160

RESULT 4
fltk3/flk-2 ligand precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C:Accession: A49265; I49347; I49346; S43290
R:Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Holl
D.; Williams, D.E.; Beckmann, M.P.
Cell 75, 1157-1167, 1993
A:Title: Molecular cloning of a ligand for the fltk3/flk-2 tyrosine kinase receptor: a
A:Reference number: A49265; MUID:94084791; PMID:7505204
A:Accession: A49265
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-231 <LYM>
A:Cross-references: GB:I23636; NID:g439441; PIDN:AAA39436.1; PID:g439442
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.
Oncogene 11, 1165-1172, 1995
A:Title: Structural analysis of human and murine fltk3 ligand genomic loci.
A:Reference number: I39075; MUID:96032581; PMID:7566977
A:Accession: I49347
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-163, 'G', 165, 'HYAG' <RES>
A:Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90952.1; PID:g1072041
A:Accession: I49346
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-197, 'L', 198-231 <RES>
A:Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040
R:Hanum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.;
felt, A.; Muench, M.; Keilner, G.; Nankawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik
Nature 368, 643-648, 1994
A:Title: Ligand for FLTK2 receptor tyrosine kinase regulates growth of haematopoietic
A:Reference number: S43290; MUID:94195428; PMID:8145851
A:Accession: S43290
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-197, 'L', 198-231 <HAN>
A:Experimental source: clone T110
A:Note: the sequence from Fig. 2c is inconsistent with that from Fig. 2a in having 4-
C:Keywords: transmembrane protein

Query Match      61.98; Score 768.5; DB 2; Length 231;
Best Local Similarity 70.38; Pred. No. 1.8e-58;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY      1 MTVALPAMSP--TTVYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVY 59
      1 MTVALPAMSPNSLLLLLLSSPLRLGTPTPCYFHSPISSNFVKFRELDTLHKLYPTV 60
Db      1 MTVALPAMSPNSLLLLLLSSPLRLGTPTPCYFHSPISSNFVKFRELDTLHKLYPTV 60
QY      60 VASNLQDEELCGGLWRLVLAQRMMERLKTVAAGSKMGLLEVRNTEIHFTVKCAFQPPSC 119
      60 VASNLQDEELCGGLWRLVLAQRMMERLKTVAAGSKMGLLEVRNTEIHFTVKCAFQPPSC 120
Db      61 VAVNLQDEELCGGLWRLVLAQRMMERLKTVAAGSKMGLLEVRNTEIHFTVKCAFQPPSC 120
QY      120 LRFVQTNISRLLOETSEQLVALKPWITR--QNSRCLLELOCCQDPDSTLLPPWSPRPLEAT 177
      120 LRFVQTNISRLLOETSEQLVALKPWITR--QNSRCLLELOCCQDPDSTLLPPWSPRPLEAT 177
Db      121 LRFVQTNISRLLOETSEQLVALKPWITR--QNSRCLLELOCCQDPDSTLLPPWSPRPLEAT 180
QY      178 APTAPQPP--LLLLLPVGLLLAAAMCLHMQRTRRTPRGEQVPPVPS 227
      178 APTAPQPP--LLLLLPVGLLLAAAMCLHMQRTRRTPRGEQVPPVPS 227

```

Db 181 ELPEPRRLDLLLLLLPLLVLAAMGLRWQARRR---GELHPGVLP 228

RESULT 5

SA3291

FLT3/FLK2 ligand (clone 7118) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999

C:Accession: SA3291

R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; K&

felt, A.; Muench, M.; Kellner, G.; Namiwawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A

Nature 368, 643-648, 1994

A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic

A:Reference number: SA3290; MUID:94195428; PMID:8145851

A:Accession: SA3291

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-220 <HMM>

Query Match 48.8%; Score 606.5; DB 2; Length 220;

Best Local Similarity 61.5%; Pred. No. 1.3e-44;

Matches 134; Conservative 18; Mismatches 43; Indels 23; Gaps 5;

QY 1 MYVLAPWSP-TTYLLLLSSGSLGTDGCFQHSPISSDFAVKIRELSYLDYLPVT 59

Db 1 MYVLAPWSPNSLLLLLSPLCLRGTPDCYFHSPISSNFKVRELTHLILKDYPT 60

QY 60 VASNLDEELCGGLMRLVLAORMERLKTAVAGSKMGLERNTETHTKCAFPQPPSC 119

Db 61 VAVNLDEELCKALMSLFLAORMIEQLKTAVAGSKMGLTLEDVNTETHTVCTFQPLPC 120

QY 120 LRFVQTNISRLQETSEOLVALKPWTR--QNFSCLELQCPDSSSTLPWPSPRP--- 173

Db 121 LRFVQTNISRLKDTQGLALKPCIGKACQNFSCLELQCPDSSSTLPWPSPRP--- 174

QY 174 ---LEATAPAPAPPLLL-----LLILPVGILLIA 201

Db 175 ATRLTATALLTVCPLLPVGTSHMFPLPFLSLSS 212

RESULT 6

I58343

flt3 ligand isoform 5H - mouse

C:Species: Mus sp. (mouse)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999

C:Accession: I58343

R:Lyman, S.D.; James, L.; Escobar, S.; Downey, H.; de Vries, P.; Brasel, K.; Stocking, K

Oncogene 10, 149-157, 1995

A:Title: Identification of soluble and membrane-bound isoforms of the murine flt3 ligand

A:Reference number: I58343; MUID:95124710; PMID:7824267

A:Accession: I58343

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-220 <RES>

A:Cross-references: GB:S76459; NID:9913479; PIDN:AAB33069.1; PID:9913480

Query Match 48.8%; Score 606.5; DB 2; Length 220;

Best Local Similarity 61.5%; Pred. No. 1.3e-44;

Matches 134; Conservative 18; Mismatches 43; Indels 23; Gaps 5;

QY 1 MYVLAPWSP-TTYLLLLSSGSLGTDGCFQHSPISSDFAVKIRELSYLDYLPVT 59

Db 1 MYVLAPWSPNSLLLLLSPLCLRGTPDCYFHSPISSNFKVRELTHLILKDYPT 60

QY 60 VASNLDEELCGGLMRLVLAORMERLKTAVAGSKMGLERNTETHTKCAFPQPPSC 119

Db 61 VAVNLDEELCKALMSLFLAORMIEQLKTAVAGSKMGLTLEDVNTETHTVCTFQPLPC 120

QY 120 LRFVQTNISRLQETSEOLVALKPWTR--QNFSCLELQCPDSSSTLPWPSPRP--- 173

Db 121 LRFVQTNISRLKDTQGLALKPCIGKACQNFSCLELQCPDSSSTLPWPSPRP--- 174

QY 174 ---LEATAPAPAPPLLL-----LLILPVGILLIA 201

Db 175 ATRLTATALLTVCPLLPVGTSHMFPLPFLSLSS 212

RESULT 7

T22672

hypothetical protein F54F12.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T22672

R:Batlow, K.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19597

A:Accession: T22672

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1217 <MIL>

A:Cross-references: EMBL:281548; NID:e1062020; PIDN:CAB04464.1; GSPDB:GN00021; CESP:F

A:Experimental source: Clone F54F12

C:Genetics:

A:Gene: CESP:F54F12.1

A:Map position: 3

A:Introns: 742/2; 826/1; 884/2; 922/3; 972/1; 1024/2; 1102/1

Query Match 7.5%; Score 93; DB 2; Length 1217;

Best Local Similarity 23.6%; Pred. No. 8;

Matches 38; Conservative 33; Mismatches 68; Indels 22; Gaps 6;

QY 83 MERLTVAGSKMGL---LELVNTEHIFVTKCAFPQPPSCIRFVQTNISRLQETSEQLV 139

Db 627 MDVAVAVDGTQYSSVIDALEKLTMDLDFQYKFKAPATLKAIDL---FFASVSNLA 682

QY 140 ALKPWTRQNFSCLELQCPDSSSTLP---PPWSPRPLEATAPAP---OPPLILL 191

Db 683 ALRQPTTSDPTAAPVPIPNKKSILNGNSPSSPPLPVPASSTPATPEESMLLYII 742

QY 192 LPVGLLLIA-----AMCLMQTRRTTRPRGEQVPVPSP 227

Db 743 GAVGGLVVALIIGVILFVFFQKKKKEDKPPD--PPAPLP 781

RESULT 8

TMBE12

74K alpha trans-inducing protein - human herpesvirus 3

C:Species: human herpesvirus 3, varicella-zoster virus

C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999

C:Accession: C27342

R:Davidson, A.D.; Scott, J.E.

J. Gen. Virol. 67, 1759-1816, 1986

A:Title: The complete DNA sequence of varicella-zoster virus.

A:Reference number: A27345; MUID:86306657; PMID:3018124

A:Accession: C27342

A:Molecule type: DNA

A:Residues: 1-661 <DAV>

A:Cross-references: EMBL:X04370; NID:959989; PIDN:CAA27895.1; PID:960001

C:Genetics:

A:Gene: 12

C:Superfamily: herpesvirus 77K alpha trans-inducing protein

C:Keywords: trans-inducing protein; transcription regulation

Query Match 7.4%; Score 92; DB 1; Length 661;

Best Local Similarity 26.6%; Pred. No. 4.9;

Matches 61; Conservative 29; Mismatches 103; Indels 36; Gaps 11;

QY 19 LLSLSLSTQDCC---FQHSPISSDFAVKT--RELSDYLDQVPVYVNSLQDEELCG- 71

Db 79 LTPVLQSTERHSHVLLGLHNNVPESLVSCMSNDVHDGEPQRYMETIQRCILDRLKSG 138

QY 72 GLMRLVLAORMMERLKTAVAGSKMGLERVN---TEIHVTKCAFP---PSCLEFV 123

Db 139 GLM-WVYENTYWOYLKTYTGADEVYSEKVKKSKSYLVLFSSVVAKKPISRHPFKSKI 197

QY 124 QTNISRLQETSQOLVALKPMITRONFSRCLEOCQPDSSSTLPPEMSP-RPLEATAPATAP 182
 Db 198 NSDRGICQICQELREALGAQOKYM--YFMR-----PDDPTNPSPDRIRIVQELAAVTAT 247
 QY 183 QPRLILLILLIPVGLILLAAACMLHMORTRRTPRPGQVPPVSPDILL 231
 Db 248 GYGMWMLFLVDVDD-----ARVCRHLKIQFRIRNGPRASV---IPDDL 287

RESULT 9

T19543

hypothetical protein C28D4.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T19543

R:McMurray, A.

Submitted to the EMBL Data Library, November 1996

A:Reference number: Z19139

A:Accession: T19543

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-474 <TIL>

A:Cross-references: EMBL:282259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2

A:Experimental source: clone C28D4

C:Genetics:

A:Gene: CESP:C28D4.2

A:Map position: 4

A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

Query Match

Best Local Similarity 7.2%; Score 89.5; DB 2; Length 474;

Matches 59; Conservative 29; Mismatches 82; Indels 75; Gaps 15;

QY 27 TQDC-----SFQHS-PISSDFAVKIREL-SDYLLQDYPVYASNLQDEELCGGLMRL 76
 Db 65 TTDCVDLKKYFSKFDSSAPISGELLFPAFLCAKYL-----GGAWRK 106
 QY 77 VLAQRMERLKTAVGSKMGGILLERVNTLHFVTKACAPPPSCUR-FVQTNISRLQERT- 134
 Db 107 VKIEEF-RIRAITGG-MSNLLFLVELPAH-LTPIQMEPKALLRVHCGSDIDQLLSFSV 162
 QY 135 -----SEQLVALKPMITRONFSRCLELOC-----QPDSSSTLPPEMSPR-PLEATA 178
 Db 163 VFTLLSRNLGPKMLGVFGGREGQFLPSRALQCLELSKSLTLAPYAVHNTLDAP1 222
 QY 179 PTAPQPPRLILLIPVGLILLAAACMLHMORTRRRP-----RPGE-----QVPPVSPQD 229
 Db 223 PKERQ-----TLQTAQWMLERF-----KTPPAGERPLEMTLTQAKVKSYPST 266
 QY 230 LLAVE 234
 Db 267 ITVAQ 271

RESULT 10

I48201

adhalin - golden hamster

C:Species: Mesocricetus auratus (golden hamster)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Jun-2000

C:Accession: I48201

R:Roberts, S.L.; Campbell, K.P.

FEBS Lett. 364, 245-249, 1995

A:Title: Adhalin mRNA and cDNA sequence are normal in the cardiomyopathic hamster.

A:Reference number: I48201; MUID:95278335; PMID:7758576

A:Accession: I48201

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-387 <RES>

A:Cross-references: EMBL:U21677; NID:g726481; PIDN:AAA81645.1; PID:g726482

C:Superfamily: mouse adhalin

Query Match

Best Local Similarity 7.2%; Score 89; DB 2; Length 387;

Matches 73.4%; Pred. No. 4.8;

Matches 71; Conservative 26; Mismatches 97; Indels 110; Gaps 14;
 QY 11 TTYILLILLSSGLSTQCCSFQHSPISSDFAVKIRELSDYLLQDYPVYASNLQDEELC 70
 Db 115 TTRQRLILLI-----EDPEGRLPYQAEFLVRSHDVEEVL-----PSTPNRFL--TAL 161
 QY 71 GGLMRL-----VLAQRMERLKTAVGSKMGGILLERVNTLHFVT-----K 110
 Db 162 GGLMELGELQILNITSALDRGRVPLPIEGRKESGYIIVGSAITPSTCLKNVASPDSTAR 221
 QY 111 CAPQPP--SC-----LRFVQTNISRLQETSQOLVALKPMITRONFSRCLELOCQD 161
 Db 222 CAQGPRLSLCYDSLAPHFRVDMCNVSLVDSKVPRLD-----EVPFGD 266
 QY 162 SSTLPPEMSPRPLEAT-----APTAPQPPRLILLIPVGLILLAAAC----- 204
 Db 267 GLEHDEFCPTPEATGRDFLADALVTLVLPVALL--TLLLAYIMCCREGQLKRD 323
 QY 205 -----LHMORTRRTPRP-----GEQVPP-VPSQD-DLL 231
 Db 324 MATSDIQWVHCTHIGNTEELRQMARKEVPRPLSTLFMFVNRIGERLPPRVDSNAQPLI 383
 QY 232 LVEH 235
 Db 384 LDQH 387

RESULT 11

S60735

splicing factor SF3a 120K chain - human

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C:Accession: S60735; S60733

R:Kremer, A.; Mulhauser, F.; Wersig, C.; Groening, K.; Billbe, G.

RNA 1, 260-272, 1995

A:Title: Mammalian splicing factor SF3a120 represents a new member of the SURP family

A:Reference number: S60733; MUID:96079958; PMID:7489498

A:Accession: S60735

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-793 <KRA>

A:Cross-references: EMBL:X85237; NID:g899297; PIDN:CAA59494.1; PID:g899298

A:Accession: S60733

A:Molecule type: protein

A:Residues: 51-62; 82-94; 270-275; 397-414; 448-463 <KRA2>

C:Genetics: A:Gene: GDB:SF3A120; PRP21; SAP114

A:Cross-references: GDB:9955873

A:Map position: 22q12.1-22qter

C:Superfamily: human splicing factor SF3a 120K chain; ubiquitin homology

C:Keywords: pre-mRNA splicing

P:714-790/Domain: ubiquitin homology <UBH>

Query Match 7.2%; Score 89; DB 1; Length 793;

Best Local Similarity 22.3%; Pred. No. 11;

Matches 67; Conservative 34; Mismatches 79; Indels 120; Gaps 17;

QY 4 LAPANSPTTYILLILLSSGLSGTQCCSFQHSPISSDFAVKIRELSDYLLQDYPVYASN 63
 Db 401 LPPAPAPDEYLV-----SPITGE--KI-----PASK 424
 QY 64 LQDELQCGILMRLVLAQRMW-RLKTV-----AGSKMGGILLERVNTLHF 107
 Db 425 MQEHKRIG-----LIDPFWMLQDRDRIKESQDDEVYAPGLDISSSLKQLAER-RDIFG 478
 QY 108 VTCA-----FQPPPSCLRF-----VQTNISRLQETSQOLVALKPMI 145
 Db 479 VEETAIKKGIEEELQKEEKVYTDGHSGMARQQAQANIT--LQQLALHKKAGLV 536
 QY 146 -----TRQNF--SRCLELOCQD-----DSSQLP-----PWSRPLEAT---APT 180
 Db 537 PEDDTKEIKIGSKNEIPQPPPPSSATNIPSSAPITSVPRPTMPPVRTTVASAVP 596

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OM protein - protein search, using sw model

Run on: November 24, 2002, 10:03:41 ; Search time 8.57296 Seconds
(without alignments)
1136.939 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242
Sequence: 1 MTVLPAWSPRYLLDLLL.....RPGQVPVPSPQDLLVEH 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	1 FLJ3_HUMAN	P49771 homo sapien
2	766	61.8	232	1 FLJ3_MOUSE	P49772 mus musculu
3	92	7.4	661	1 AT12_VZVD	P09264 varicella-2
4	89.5	7.2	941	1 GBR2_HUMAN	075899 homo sapien
5	89	7.2	387	1 SGCA_MESAU	064555 mesocricetu
6	89	7.2	793	1 S3A1_HUMAN	054559 homo sapien
7	87.5	7.0	415	1 TNR3_MOUSE	P50284 mus musculu
8	87.5	7.0	479	1 MPIP_DROME	P20483 drosophila
9	87	7.0	910	1 DDRI_RAT	063474 rattus norv
10	87	7.0	911	1 DDRI_MOUSE	063474 rattus norv
11	86.5	7.0	1394	1 CNCA_BOVIN	028181 bos taurus
12	86	6.9	485	1 SSGP_VOLCA	P21997 volvox cart
13	85	6.8	282	1 ATFS_HUMAN	09Y281 homo sapien
14	85	6.8	366	1 FCCN_RAT	P13599 rattus norv
15	84.5	6.8	3726	1 ABFI_MOUSE	061329 mus musculu
16	84	6.8	582	1 MNT_HUMAN	099593 homo sapien
17	84	6.8	1234	1 YF48_HUMAN	09hcm4 homo sapien
18	84	6.8	1234	1 NPHN_RAT	09hcm4 rattus norv
19	83.5	6.7	671	1 Z282_HUMAN	09udv7 homo sapien
20	83	6.7	758	1 VKGC_HUMAN	P38435 homo sapien
21	82	6.6	2167	1 SHK1_RAT	09wv48 rattus norv
22	81.5	6.6	488	1 MMT1_HUMAN	P24347 homo sapien
23	81.5	6.6	591	1 MNT_MOUSE	008789 mus musculu
24	81.5	6.6	2124	1 Y192_HUMAN	093074 homo sapien
25	81	6.5	283	1 ATFS_MOUSE	070101 mus musculu
26	81	6.5	387	1 SGCA_MOUSE	P82350 mus musculu
27	81	6.5	428	1 EPC_HUMAN	P01854 homo sapien
28	81	6.5	1248	1 DIAL_HUMAN	060610 homo sapien
29	80.5	6.5	1402	1 IF4G_RABIT	P41110 oryctolagus
30	80	6.4	397	1 CEFD_STRCL	P18549 streptomyces
31	80	6.4	940	1 GBR2_RAT	088871 rattus norv
32	80	6.4	1174	1 KPCI_COCHF	042632 cochlidoth
33	80	6.4	1794	1 YAV1_SCHPO	Q10172 schizosacch

ALIGNMENTS

RESULT 1	FLJ3_HUMAN	STANDARD;	PRT;	235 AA.
AC	P49771;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3 ligand) (Flt3l).			
DE	FLT3LG.			
GN	FLT3LG.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94195428; PubMed=8145851;			
RA	Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S., Bazen J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J., Duda G., Martina N., Peterson D., Menon S., Shanafelt A., Muench A., Rosnet G., Namioka R., Kennick D., Roncarolo M.G., Zlotnick A., Rosnet G., Dubreuil P., Birbaum D., Lee F.;			
RT	"Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic stem cells and is encoded by variant RNAs.";			
RL	Nature 368:643-648(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94235842; PubMed=8180375;			
RA	Lymon S.D., James L., Johnson L., Brasel K., de Vries P., Escobar S.S., Downey H., Splet R.R., Beckmann M.P., McKenna H.J.;			
RT	"Cloning of the human homologue of the murine flt3 ligand: a growth factor for early hematopoietic progenitor cells.";			
RL	Blood 83:2795-2801(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.			
RX	MEDLINE=96032581; PubMed=7566977;			
RA	Lymon S.D., Stocking K., Davison B., Fletcher F., Johnson L., Escobar S.;			
RT	"Structural analysis of human and murine flt3 ligand genomic loci.";			
RL	Oncogene 11:1165-1172(1995).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).			
RX	MEDLINE=20343011; PubMed=10881197;			
RA	Savvides S.N., Boone T., Karplus P.A.;			
RT	"Flt3 ligand structure and unexpected commonalities of helical bundles and cysteine knots.";			
RL	Nat. Struct. Biol. 7:486-491(2000).			
CC	- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING FACTORS AND INTERLEUKINS.			
CC	- SUBUNIT: Homodimer (isoform 2).			
CC	- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1); secreted (isoform 2).			
CC	- ALTERNATIVE PRODUCTS: 2 isoforms; a 1/membrane-bound (shown here) and 2/soluble; are produced by alternative splicing.			

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DR EMBL; U04806; AAA17999.1; -;
 DR EMBL; U03858; AAA19825.1; -;
 DR EMBL; U29874; AAA90949.1; -;
 DR EMBL; U29874; AAA90950.1; -;
 DR PDB; 1ETE; 09-JUN-00.
 DR GeneW; HGNC:3766; FLT3LG.
 DR MIM; 600007; -;
 DR InterPro; IPR004213; Flt3_lig.
 DR Pfam; PF02947; Flt3_lig; 1.
 KW Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal; 3D-structure.

FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 235 SL CYTOKINE.
 FT DOMAIN 27 184 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 185 205 POTENTIAL.
 FT DOMAIN 206 235 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 30 111
 FT DISULFID 70 153
 FT DISULFID 119 158
 FT CARBOHYD 126 126
 FT CARBOHYD 149 149
 FT VARSPPLIC 161 178
 FT VARSPPLIC 179 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SQUENCE 235 AA; 26416 MW; 73B95BF693B4C6CF CRC64; MISSING (IN ISOFORM 2).
 G -> A (IN REF. 1).

Query Match 100.0%; Score 1242; DB 1; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1,le-96;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLLSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
 DB 1 MTVLAPAMSPPTTYLLLLLSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
 QY 61 ASNLODELCGGMLRVLVLAQRMERLKTVAAGSMOGLLEVRNTEHFVTKCAFQPPSCL 120
 DB 61 ASNLODELCGGMLRVLVLAQRMERLKTVAAGSMOGLLEVRNTEHFVTKCAFQPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKFWITRONFSRCLTEQCQPDSTLPPSPRLKATATP 180
 DB 121 RFVQTNISRLQETSEQLVALKFWITRONFSRCLTEQCQPDSTLPPSPRLKATATP 180
 QY 181 APQPELLLLLVGLLLAAAWCLMQRTRRRTPRGQVPPVPQDLLVEH 235
 DB 181 APQPELLLLLVGLLLAAAWCLMQRTRRRTPRGQVPPVPQDLLVEH 235

RESULT 2
 FL3L_MOUSE STANDARD: PRT: 232 AA.
 AC P49772; 064085;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE SL cytokine precursor (fms-related tyrosine kinase 3 ligand) (Flt3 ligand) (Flt3).
 GN FLT3LG OR FLT3L.
 OS Mus musculus (Mouse).
 OC Mammalia; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94195428; PubMed=8145851;

RA Hannum C., Culpepper J., Campbell D., McLanahan T., Zurawski S.,
 RA Bazar J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J.,
 RA Duda G., Martina N., Peterson D., Meon S., Shanafelt A.,
 RA Wuensch M., Kellner G., Nemikawa R., Rennick D., Rocco M.G.,
 RA Zlotnik A., Rosnet O., Dubreuil P., Birbaun D., Lee F.,
 RA "Ligand for Flt3/Flk2 receptor tyrosine kinase regulates growth of
 RT haematopoietic stem cells and is encoded by variant RNAs.";
 RL Nature 368:643-648(1994).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-SJL/J;
 RX MEDLINE=94084791; PubMed=7505204;
 RA Lyman S.D., James L., Vandenbos T., Devries P., Brasel K.,
 RA Gliniak B., Hollingsworth L.T., Picha K.S., McKenna H.J.,
 RA Spielt R.R., Fletcher F.A., Markosky E., Farrar T.,
 RA Foxworth D., Williams D.E., Beckmann M.P.;
 RT "Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase
 RT receptor: a proliferative factor for primitive hematopoietic cells.";
 RL Cell 75:1157-1167(1993).
 RN [3]
 RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RP MEDLINE=96032581; PubMed=7566977;
 RX Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
 RA Escobar S.;
 RT "Structural analysis of human and murine flt3 ligand genomic loci.";
 RL Oncogene 11:1165-1172(1995).
 RN [4]
 RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RP MEDLINE=95124710; PubMed=7824267;
 RX Lyman S.D., James L., Escobar S., Downey H., de Vries P.,
 RA Brasel K., Stocking K., Beckmann M.P., Copeland N.G.,
 RA Cleveland L.S.;
 RT "Identification of soluble and membrane-bound isoforms of the murine
 RT flt3 ligand generated by alternative splicing of mRNAs.";
 RL Oncogene 10:149-157(1995).
 RN [5]
 RN SEQUENCE FROM N.A.
 RA McLanahan T., Culpepper J., Campbell D., Wagner J.,
 RA Franz-Bacon K., Mattson J., Tsai S., Luh J., Gutierrez M.J.,
 RA Matzel M.G., Rosnet O., Birbaun D., Hannum C.;
 RL Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.
 CC -I- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC
 CC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING
 CC FACTORS AND INTERLEUKINS.
 CC -I- SUBUNIT: Homodimer (soluble isoform) (By similarity).
 CC -I- SUBCELLULAR LOCATION: Type 1 membrane protein. Two soluble
 CC isoforms are also produced by alternative splicing. One of which,
 CC isoform 3/E6, is biologically active, while the other, isoform
 CC 4/E6delta16, is inactive.
 CC -I- ALTERNATIVE PRODUCTS: 4 isoforms; 1/6C (shown here), 2/5H, 3/E6
 CC and 4/E6delta16; are produced by alternative splicing.
 CC -----
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Query Match	61.8%	Score 768	DB 1	Length 232
Best Local Similarity	70.0%	Pred. No.	3.6e-57	
Matches 163	Conservative 17	Mismatches 43	Indels 10	Gaps 4

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CC CC      RESULT 3
CC CC      AT12_VZVD
CC AC      ID       AT12_VZVD          STANDARD:    PRT;        661 AA.
CC AC      P09264;
CC DT      01-MAR-1989 (Rel. 10, Created)
CC DT      01-MAR-1989 (Rel. 10, Last sequence update)
CC DT      01-NOV-1990 (Rel. 16, Last annotation update)
CC DE      Alpha trans-inducing factor 74 kDa protein.
CC GN      12.
CC OS      Varicella-zoster virus (strain Dumas) (VZV).
CC OC      Viruses: dsDNA viruses, no RNA stage; Herpesviridae;
CC OX      Alphaherpesvirinae; Varicellovirus.
CC RN      NCBI_TaxID=10338;
CC RP      [1]
CC RX      SEQUENCE FROM N.A.
CC RL      MEDLINE=86306657; PubMed=3018124;
CC RA      Davidson A.J., Scott J.E.;
CC RT      "The complete DNA sequence of varicella-zoster virus.";
CC RL      J. Gen. Virol. 67:1759-1816(1986).
CC CC      -I- FUNCTION: MODULATE ALPHA TRANS-INDUCING FACTOR-DEPENDENT
CC CC      ACTIVATION OF ALPHA GENES.
CC CC      -----
CC CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC CC      use by non-profit institutions as long as their content is in no way
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CC CC      or send an email to license@isb-sib.ch).
CC CC      -----

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Query Match	7.48;	Score 92;	DB 1;	Length 661;
Best Local Similarity	26.68;	Pred. No. 2.7;		
Matches 61;	Conservative 29;	Mismatches 103;	Indels 36;	Gaps 11;

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QY      183 QPRLTLLLVGLLLLAAMCLHWRTTRTPRPGEQVPVPSQDLL 231
      : | | | | | | | | | | | | | |
Db      248 GYGMMLFELDVD----ARVCRHLKLQFRIRIGPRASV----IPDDL 287

```

RP SEQUENCE FROM N.A. (ISOFORM 2A).
RC TISSUE=Cerebellum;
RX MEDLINE=99087321; PubMed=9872316;
RA White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H.,
RA Barnes A.A., Emson P., Foord S.M., Marshall F.H.;
RT "Heterodimerization is required for the formation of a functional
RT GABA(B) receptor.";
RL Nature 396:679-682(1998).
RN [2].
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2A, 2B AND 2C).
RN TISSUE=Brain;
RC MEDLINE=20193514; PubMed=10727622;
RX Clark J.A., Mezey E., Lam A.S., Bonner T.I.;
RA "Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";
RL Brain Res. 860:41-52(2000).
RN [3].
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RA Liu M., Parker R., McCrea K., Watson J., Baker E., Sutherland G.,
RA Herzog H.;
RT "Cloning and characterization of a novel human GABA-B receptor subtype
RT with high affinity for GABA and low affinity for Baclofen.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [4].
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RC TISSUE=Hippocampus;
RX Borowsky B., Laz T., Gerald C.;
RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL [5].
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RN

RC TISSUE-Fetal brain;
RX MEDLINE-99189236; PubMed-10087195;
RA Ng G.Y.K., McDonald T., Bonnett T., Rigby M., Heavens R., Whiting P.,
RA Chateauf A., Coulombe N., Kargman S., Caskey T., Evans J.F.,
RA O'Neill G.P., Liu Q.,
RT "Cloning of a novel G-protein-coupled receptor GPR 51 resembling GABAB
RT receptors expressed predominantly in nervous tissues and mapped
RT proximal to the hereditary sensory neuropathy type 1 locus on
RT chromosome 9.";
RL Genomics 56:288-295(1999).
RN [6].
RP SEQUENCE FROM N.A. (ISOFORM 2A), AND VARIANTS PHE-628 AND ALA-869.
RC TISSUE-Brain;
RX MEDLINE-99263199; PubMed-10328880;
RA Martin S.C., Russek S.J., Farb D.H.;
RT "Molecular identification of the human GABABR2: cell surface
RT expression and coupling to adenylyl cyclase in the absence of
RT GABABR1.";
RL Mol. Cell. Neurosci. 13:180-191(1999).
RN [7].
RP R1A-R2 INTERACTION.
RX MEDLINE-99175124; PubMed-10075644;
RA Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan R.,
RA Kargman S., Chateauf A., Tsukamoto N., McDonald T., Whiting P.,
RA Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
RA Bonner T.I., O'Neill G.P.;
RT "Identification of a GABAB receptor subunit, gb2, required for
RT functional GABAB receptor activity.";
RL J. Biol. Chem. 274:7607-7610(1999).
RN [8].
RP R1A-R2 INTERACTION.
RX MEDLINE-20237752; PubMed-10773016;
RA Sullivan R., Chateauf A., Coulombe N., Kolakowski L.F. Jr.,
RA Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K.,
RA Abramovitz M., O'Neill G.P., Ng G.Y.K.;
RT "Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B))
RT receptors with truncated receptors and metabotropic glutamate
RT receptor 4 supports the GABA(B) heterodimer as the functional
RT receptor.";
RL J. Pharmacol. Exp. Ther. 293:460-467(2000).
RN [9].
RP -1- FUNCTION FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES
CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
CC ANTINOCICEPTION.
CC -1- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
CC HAPPEN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
CC PLASMA MEMBRANE.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: 2A (SHOWN HERE), 2B AND 2C; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN
CC CEREBRAL CORTEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AND
CC TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY CORPUS
CC CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, AMYGDALA AND MEDULLA.
CC WEAKLY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE.
CC -1- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC GABA-B RECEPTOR SUBFAMILY.
CC -----

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CC -----
DR EMBL, AJ012188; CA09942.1; -
DR EMBL, AF056085; AAC63228.1; -
DR EMBL, AF095723; AAC63383.1; -
DR EMBL, AF095724; AAC63384.1; -
DR EMBL, AF095784; AAD30389.1; -
DR EMBL, AF074483; AAD03336.1; -
DR EMBL, AF069755; AAC99345.1; -
DR EMBL, AF099033; AAD45867.1; -
DR Genew, HGNC:4507; GPR51.
DR InterPro, IPR001828; ANF_receptor.
DR InterPro, IPR000337; GPCR_Mgr.
DR Pfam, PF00003; 7tm.3; 1.
DR Pfam, PF01094; ANF_receptor; 1.
DR PROSITE, PS00979; G-PROTEIN_RECPE_F3.1; FALSE_NEG.
DR PROSITE, PS00980; G-PROTEIN_RECPE_F3.2; FALSE_NEG.
DR PROSITE, PS00981; G-PROTEIN_RECPE_F3.3; FALSE_NEG.
DR PROSITE, PS0259; G-PROTEIN_RECPE_F3.4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Postsynaptic membrane; Coiled coil; Alternative splicing;
KW Polymorphism.
KM SIGNAL 1 41
FT CHAIN 42 941
FT FT
FT DOMAIN 42 483
FT TRANSMEM 484 504
FT DOMAIN 505 522
FT TRANSMEM 523 543
FT DOMAIN 544 551
FT TRANSMEM 552 572
FT DOMAIN 573 597
FT TRANSMEM 598 618
FT DOMAIN 619 654
FT TRANSMEM 655 675
FT DOMAIN 676 691
FT TRANSMEM 692 712
FT DOMAIN 713 720
FT TRANSMEM 721 741
FT DOMAIN 742 941
FT DOMAIN 781 819
FT CARBOHYD 90 90
FT CARBOHYD 298 298
FT CARBOHYD 389 389
FT CARBOHYD 404 404
FT CARBOHYD 453 453
FT VARSPLIC 902 927
FT VARIANT 929 941
FT FT
FT VARIANT 628 628
FT FT
FT VARIANT 869 869
FT FT
FT CONFLICT 6 6
FT CONFLICT 12 12
FT CONFLICT 424 424
SQ SEQUENCE 941 AA; 105821 MW; 09F1773DB0673C5D CRC64;
Query Match 7.28; Score 89.5; DB 1; Length 941;
Best local similarity 44.18;
Matches 26; Conservative 2; Mismatches 22; Indels 9; Gaps 3;
Oy 170 SPRPLEATAPAPDP-----LILLILLPVGLLLAAMCWMQRTRRTRRPEGEQVPV 224
Db 3 SPKSGGPGPPPPPPPPPARLLLLPLLLPLAPGAW--GW--ARGAPPPSPPL 56

[illegible]

ID	NAME	STANDARD	PRT	793 AA
Db	162 G6WELGELQTLNITSALDRGRVPLIEGRKEGVYIKVSGATFPFSLKMWASPSDYAR			221
Qy	111 CAFOPP--SC-----LRFVQNTISFLQETSEQLVALKPWITRONFSKLELOACPD			161
Db	222 GAGGPPPLSLSCYDSLAPHFHVDWCNVSLSVDSKVEPEILD-----EVPKPGD			266
Qy	162 SSTLPKPSRPRLKAT-----APTAQPPRLLLLLLPVGLLLLAANC-----			204
Db	267 GLEHDPFPCPEPTKATGDFLADALVLLVLLVALLL---TLLTALYKCCRREGOLKRD			333
Qy	205 -----LHMORTRRPRP-----GEVOPV-VPSPQ-DLL			231
Db	324 MATSDIQWVHCTIIGNTEELRQMAAREVPRPLSTLPMENVKRGELPRPRVDSAQVPLI			383
Qy	232 LVKH 235			
Db	384 IDQH 387			
RESULT 6				
S3AL_HUMAN				
ID	S3AL_HUMAN	STANDARD:	PRT:	793 AA.
AC	Q15459.			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Splicing factor 3 subunit 1 (Spliceosome associated protein 114) (SAP 114) (SF3a120).			
GN	SF3A1 OR SAP114.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxId=9606;			
RP	[1]			
RE	SEQUENCE FROM N.A.			
RX	MEDLINE=96079958; PubMed=7489498;			
RT	"Mammalian splicing factor SF3a120 represents a new member of the SUP family of proteins and is homologous to the essential splicing factor PR22p of Saccharomyces cerevisiae.";			
RL	RNA 1:260-272(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20057165; PubMed=10591208;			
RA	Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,			
RA	Clamp M., Smink L.J., Atscough R., Almeida J.P., Babbage A.K.,			
RA	Baiguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,			
RA	Bird C.P., Blakey S.E., Brideman A.M., Buck D., Burgess J.,			
RA	Burill W.D., Burton J., Carter C., Carter N.P., Chen Y., Clark G.,			
RA	Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,			
RA	Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,			
RA	Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,			
RA	Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,			
RA	Gilbert J.G.R., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C.,			
RA	Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,			
RA	Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,			
RA	Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,			
RA	Matyln J.D., Meshreghi-Mohammadi M., Matthews L.H., Mccann O.T.,			
RA	Mcclay J., McLaren S., Mcmurray A.A., Milne S.A., Mortimore B.J.,			
RA	Odeli C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.			
RA	Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L.,			
RA	Scott C.E., Sehna H.K., Skuce C.D., Smalley S., Smith M.L.,			
RA	Soderlund C., Spraeon L., Steward C.A., Sulston N.J., Swann R.M.,			
RA	Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,			
RA	Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilmng L.,			
RA	Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers S., Shimizu N.,			
RA	Mioshimia S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,			
RA	Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyma S.,			
RA	Roe B.A., Chen F., Chu L., Crabtree J., Descamps S., Do A., Do T.,			
RA	Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,			
RA	Lewis J., Lewis S., Lin S.-P., Loh P., Malay J.E., Nguyen T., Pan H.,			
RA	Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaui S., Sloan D., Song L.,			
RA	Wang Q., Wang Y., Wang Z., White Z., Willingham D., Wu H., Yao Z.,			

RA Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
RA Fulcon R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozerisky P., Rohlfing T.,
RA Schet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
RA Emanuel B.S., Shikh T., Kurahashi H., Saitta S., Budarf M.L.,
RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
RA Kim U.J., Shizuya H., Simon M.L., Dunamski J.P., Feyzadi M., Kedra D.,
RA Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
RA Tilahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
- [3]
RN CHARACTERIZATION OF THE SPLICEOSOME.
RX MEDLINE=20337962; PubMed=10882114;
RA Das R., Zhou Z., Reed R.;
RT "Functional association of U2 snRNP with the ATP-independent
RT spliceosomal complex E";
RL Mol. Cell 5:779-787(2000).
- [1- FUNCTIONAL ASSOCIATION OF THE SPLICING FACTOR SF3A REQUIRED FOR 'A'
CC COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE
CC BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT
CC BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS
CC ESSENTIAL. IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE
CC INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX.
- [1- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3A WHICH IS COMPOSED OF
CC THREE SUBUNITS: SF3A3/SAP61, SF3A2/SAP62, SF3A1/SAP114. SF3A
CC ASSOCIATES WITH THE SPLICING FACTOR SF3B AND A 12S RNA UNIT TO
CC FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX (U2 SNRNP).
CC INTERACTS WITH SF3A3.
- [1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC [1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.
CC [1- SIMILARITY: CONTAINS 1 UBQUITIN-LIKE DOMAIN.
CC [1- SIMILARITY: TO YEAST PRE-MRNA SPLICING FACTOR PRP21.
- [1- SIMILARITY: TO YEAST PRE-MRNA SPLICING FACTOR PRP21.
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DR EMBL: X85237; CAAS9494.1; -
DR EMBL: AC004997; AAC23435.1; -
DR HSSP: Q15843; IND.
DR Genew: HGNC:10765; SF3A1.
DR MIM: 605595; -
DR InterPro: IPR000061; Surp.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00240; Ubiquitin; 1.
DR Pfam: PF01805; Surp; 2.
DR SMART: SM00213; UBO; 1.
DR PROSITE: PS50053; UBQUITIN_2; 1.
KM Slicesome; mRNA processing; mRNA splicing; Nuclear protein; Repeat.
FT REPEAT 52 94 SURP MOTIF 1.
FT REPEAT 166 208 SURP MOTIF 2.
FT DOMAIN 707 793 UBQUITIN-LIKE.
FT DOMAIN 10 16 POLY-PRO.
FT DOMAIN 118 122 POLY-GLU.
FT DOMAIN 260 267 POLY-GLU.
FT DOMAIN 369 372 POLY-PRO.
FT DOMAIN 557 560 POLY-PRO.
FT DOMAIN 672 675 POLY-PRO.
SQ SEQUENCE 793 AA: 88886 MW: 72591 EC4577305C CRC64;

Query Match 7.2%; Score 89; DB 1; Length 793;
Best Local Similarity 22.3%; Pred. No. 5.8; Mismatches 17;
Matches 67; Conservative 34; Indels 120; Gaps 17;
4 LAPAWSPTVLLILLISGLSTGDCSFQHSPISSDFAVKIRLSLDYDPTVAVSN 63

Db 401 LPPAPADEVLY-----SPITGE--KI-----PASK 424
Qy 64 LDEELCGGLRLVLAORME-RLKTV-----AGSKMOGLLEVNTEIHF 107
Db 425 MOENRIG-----ILDRPFEORDRSIREKOSDEVYAPGLDISSIKQALER-RTDIFG 478
Qy 108 VTKCA-----FOPPSCLAR-----VQTNISRLLOETSEQLVAKPMI 145
Db 479 VEEFAIGKKIGEEITQKPEEKVWDGSGSMARQQAQANIT--LQEQIEAIHKAGLV 536
Qy 146 ----TRONF--SRCLERQCP-----DSSTLP-----PPWSRPLEAT---APT 180
Db 537 PEDDTKEIGSKNEIIPQPPPSATINIPSSAPITSVPRPTMPPTVTSVAVPY 596
Qy 181 APQPLLILLIPVGLILLAAACLIHQRR-----RTPRGEVPP--VPSR 227
Db 597 MPRPPMASVRLPPGSAVIAWPPILIHARINVVMPSPADPIMAPRPPMIVTAVPAP 656
RESULT 7
TNR3_MOUSE STANDARD: PRT; 415 AA.
ID TNR3_MOUSE
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 3 precursor
GN (Lymphotoxin-beta receptor).
DB LTRB OR TNFRSF3 OR TNFCR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CVB; TISSUE=Lung;
RX MEDLINE=96072804; PubMed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.;
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression.";
RL J. Immunol. 155:5280-5288(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163885; PubMed=8586432;
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA Honjo T.;
RT "The murine lymphotoxin-beta receptor cDNA: Isolation by the signal
RT sequence trap and chromosomal mapping.";
RL Genomics 30:312-319(1995).
CC [1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC LTR and LTB, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
CC and TRAF5. May play a role in the development of lymphoid organs
CC (By similarity).
CC [1- SUBUNIT: Self-associates (By similarity).
CC [1- SUBCELLULAR LOCATION: Type I membrane protein.
CC [1- SIMILARITY: CONTAINS 4 TNR-CYS REPEATS.

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DR EMBL: U29173; AAA68964.1; -
DR EMBL: L38423; AAB00846.1; -
DR EMBL: U30798; AAB81334.1; -
DR HSSP: Q14763; IDOG.
DR MGI: MGI:104875; Ltrb.
DR InterPro: IPR001368; TNR_C6.

RT identifies two cell cycle genes from *Drosophila*: a *cdc2* homologue and
RT string "1.9:3565-3571(1990).
RL EMBO J. 9:3565-3571(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Suton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Beeson R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bellow K.Y., Benos P.V., Bertoni B.P., Bhandari D., Bolintiner S.,
RA Borokova D., Botchan M.R., Bouck J., Brooksstein P., Brothier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Centar A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Paulos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Moore S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flogel C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Godar A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.D., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegam C.,
RA Jitali M.B., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon R., Nuskern D.R., Pacleby J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svaykdas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.N., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster* ";
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: THIS PROTEIN FUNCTIONS AS A DOSE-DEPENDENT INDUCER IN
CC MITOTIC CONTROL. IT IS A TYROSINE PROTEIN PHOSPHATASE REQUIRED FOR
CC PROGRESSION OF THE CELL CYCLE. IT MAY DIRECTLY DEPHOSPHORYLATE
CC P34(CDC2) AND ACTIVATE THE P34(CDC2) KINASE ACTIVITY.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SIMILARITY: BELONGS TO THE MPI PHOSPHATASE FAMILY.
CC -1- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
CC -----
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CC -----
CC EMBL: M24909; AAA28916.1; -
DR EMBL: X57495; CAA40732.1; -
DR EMBL: AE003768; AAF56885.1; -
DR PIR: A33290; A33290.
DR PIR: S12008; S12008.
DR HSP: P30304; ICG5.
DR Flybase: FBgn0003525; stg.
DR InterPro: IPR000751; MPI_Phosphatase.
DR InterPro: IPR001763; Rhodanese-like.
DR Pfam: PF00581; Rhodanese; 1.
DR PRINTS: PR00716; MPiPHPTASE.

DE DDR) (Discoïdin receptor tyrosine kinase) (Protein-tyrosine kinase
 GN MPK-6)
 GN DDR1 OR EDDR1 OR CAK OR MPK6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RP [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN=C57BL/6;
 RX MEDLINE=96204002; PubMed=8622863;
 RA Perez J.L., Jing S.O., Wong T.W.;
 RT "Identification of two isoforms of the Cak receptor kinase that are
 RT coexpressed in breast tumor cell lines."
 RL Oncogene 12:1469-1477(1996).
 RN [2]
 RP SEQUENCE OF 766-822 FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Embryonic brain;
 RX MEDLINE=93096484; PubMed=1281307;
 RA Giaraldi-Hebenstreit P., Nieto M.A., Frahn M., Mattei M.-G.,
 RA Chetlier A., Wilkinson D.G., Charney P.;
 RT "An Eph-related receptor protein tyrosine kinase gene segmentally
 RT expressed in the developing mouse hindbrain."
 RL Oncogene 7:2499-2506(1992).
 CC -1- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND
 CC RECOGNITION (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CAK I (SHOWN HERE) AND CAK II;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER BY THE
 CC ABSENCE OF A 37 RESIDUES SEGMENT.
 CC -1- TISSUE SPECIFICITY: THE PREDOMINANT ISOFORM CAK I, IS EXPRESSED IN
 CC DEVELOPING EMBRYO AND ADULT BRAIN; CAK II IS EXPRESSED IN VARIOUS
 CC EPITHELIAL CELLS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
 CC RECEPTOR SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
 CC -----
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 CC -----
 DR EMBL, L57509; AAB05209.1; -;
 DR EMBL, X57240; CAA40516.1; -;
 DR PIR, S30502; S30502.
 DR HSSP, P00523; 2PTRK.
 DR MGI, MGI:99216; Ddrl.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000421; FAS5_C.
 DR InterPro: IPR002011; RTkinasel.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam, PF00754; F5_F8_type_C; 1.
 DR ProDom, PD000001; Euk_pkinase; 1.
 DR SMART, SM00231; FAS5C; 1.
 DR SMART, SM00219; TYRC; 1.
 DR PROSITE, PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE, PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE, PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE, PS00239; RECEPTOR_TYR_KIN_II; 1.
 DR PROSITE, PS01285; FAS5C_1; 1.
 DR PROSITE, PS01286; FAS5C_2; 1.
 DR Transferrase; Tyrosine-protein kinase; Glycoprotein; Signal;
 KM Phosphorylation; Transmembrane; Receptor; ATP-binding;
 KM Alternative splicing.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 911 EPITHELIAL DISCOIDIN DOMAIN RECEPTOR 1.
 FT DOMAIN 20 414 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 415 441 POTENTIAL.
 FT DOMAIN 442 911 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 32 186 F5/8 TYPE C (PHOSPHOLIPID-BINDING,
 FT POTENTIAL).
 FT DOMAIN 379 413 GLY/PRO-RICH.
 FT DOMAIN 474 599 GLY/PRO-RICH.
 FT DOMAIN 608 903 PROTEIN KINASE.
 FT NP_BIND 614 622 ATP (BY SIMILARITY).
 FT BINDING 653 653 ATP (BY SIMILARITY).
 FT ACT_SITE 764 764 ATP (BY SIMILARITY).
 FT DISULFID 32 186 BY SIMILARITY.
 FT MOD_RES 511 511 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 790 790 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 794 794 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 795 795 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 213 213 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 372 372 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSPLIC 503 539 MISSING (IN ISOFORM CAK II).
 SQ SEQUENCE 911 AA; 101160 MW; DBB7FE03DD79510 CRC64;
 Query Match 7.0%; Score 87; DB 1; Length 911;
 Best Local Similarity 24.5%; Pred. No. 10;
 Matches 38; Conservative 12; Mismatches 35; Indels 70; Gaps 9;
 QY 143 PWIRNQRNRCLEQCQPDSTLPP-PW---SPPLPATA---PTAPOP----- 184
 Db 357 PWLFFSELSFSD-VNDSSTFPAPWPPGPPPTWFSLELEPKQGVAAKESPPRA 415
 QY 185 -----PLLLLLPVGLLLAAACLHWOR---TRRR-----T 214
 Db 416 ILICLVAIIILLILLITALLM-----WRLHWRRLSKAERVLBEELTVHLSVPGDITLLN 471
 QY 215 PRGEQVPP-----VPSPDILL 232
 Db 472 NRPGREPPYQEPFRGTPPHSAPCVNGSALL 506
 RESULT 11
 CNCG4_BOVIN STANDARD; PRT; 1394 AA.
 AC Q281B1; Q28082; Q03861;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 240 kDa protein of rod photoreceptor CNG-channel [contains: Glutamic
 DE acid-rich protein (GARP); Cyclic nucleotide-gated cation channel
 DE (CNG channel 4) (CNG-4) (Cyclic nucleotide-gated cation channel
 DE modulatory subunit)].
 DE CNGB1 OR CNCG4.
 GN CNGB1 OR CNCG4.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RP MEDLINE=96009859; PubMed=7546742;
 RX Koerschen H.G., Illing M., Seifert R., Sesti F., Williams A.,
 RA Getzes S., Colville C., Mueller F., Dose A., Godde M., Molday L.,
 RA Kaupp U.B., Molday R.S.;
 RT "A 240 kDa protein represents the complete beta subunit of the cyclic
 RT nucleotide-gated channel from rod photoreceptor."
 RL Neuron 15:627-636(1995).
 RN [2]
 RP SEQUENCE OF 454-1394 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=96198098; PubMed=8626431;
 RA Biel M., Zong X., Ludwig A., Sauter A., Hofmann F.;
 RT "Molecular cloning and expression of the modulatory subunit of the
 RT cyclic nucleotide-gated cation channel."
 RL J. Biol. Chem. 271:6349-6355(1996).

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OM protein - protein search, using sw model

Run on: November 24, 2002, 10:08:21 ; Search time 26.2232 Seconds
(without alignments)
1846.499 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242
Sequence: 1 MTVLAPAWSPTTYLLILL.....RPGQVPPVPSQDLLVEH 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP:archaea:*
2: SP:bacteria:*
3: SP:fungi:*
4: SP:human:*
5: SP:invertebrate:*
6: SP:mammal:*
7: SP:mhc:*
8: SP:organelle:*
9: SP:phage:*
10: SP:plant:*
11: SP:rodent:*
12: SP:virus:*
13: SP:vertebrate:*
14: SP:unclassified:*
15: SP:rvirus:*
16: SP:bacteriaph:*
17: SP:archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	895.5	72.1	294	6 O9MZV0	O9mzv0 canis famli
2	894.5	72.0	291	6 O9MZU9	O9mzu9 felis silve
3	840	67.6	292	6 O9GKE0	O9gke0 bos taurus
4	835	67.2	292	6 O8WNW1	O8wnw1 bos taurus
5	746	60.1	274	6 O9GKD9	O9gkd9 bos taurus
6	602.5	48.5	172	11 O61104	O61104 mus musculi
7	578	46.5	169	11 O8VCH4	O8vch4 mus musculi
8	112.5	9.1	579	10 O91G68	O91g68 oryza sativ
9	104.5	8.4	668	5 O9GK11	O9gk11 leishmania
10	102.5	8.3	648	5 O9GY33	O9gy33 leishmania
11	100.5	8.1	1809	11 O8VIR6	O8vir6 mus musculi
12	98.5	7.9	345	5 O9N753	O9n753 leishmania
13	95.5	7.7	1240	12 O9DMH8	O9dmh8 rat cytomeg
14	93.5	7.5	658	10 O9C5T0	O9c5t0 arabidopsis
15	93	7.5	1217	5 O17889	O17889 caenorhabdi
16	92.5	7.4	387	11 O8VD70	O8vd70 mus musculi

17	92.5	7.4	560	5 O9GYA1	O9gya1 leishmania
18	92.5	7.4	1400	5 O8S2S7	O8s2s7 drosophila
19	92	7.4	251	4 O9HAD2	O9had2 homo sapien
20	90.5	7.3	536	5 O9GYA0	O9gya0 leishmania
21	90.5	7.3	660	5 O9GY15	O9gy15 leishmania
22	90.5	7.3	5120	13 O9PU36	O9pu36 gallus gall
23	89.5	7.2	474	5 O17610	O17610 caenorhabdi
24	88.5	7.1	238	16 O8YWX3	O8ywx3 anabaena sp
25	88.5	7.1	270	4 O9UMT1	O9umt1 homo sapien
26	88.5	7.1	404	10 O9AMJ4	O9amj4 oryza sativ
27	88.5	7.1	1267	10 O9A3D5	O9a3d5 oryza sativ
28	88.5	7.1	1386	4 O75064	O75064 homo sapien
29	88	7.1	250	6 O9GKE2	O9gke2 sus scrofa
30	88	7.1	675	11 O9DBT2	O9dbt2 mus musculi
31	88	7.1	753	12 O56971	O56971 kennedyia ye
32	87.5	7.0	470	10 O9LUI1	O9lui1 arabidopsis
33	87.5	7.0	946	10 O22015	O22015 cyllindroche
34	87	7.0	510	5 O4A018	O4a018 leishmania
35	87	7.0	5317	5 O8TA74	O8ta74 hemientrot
36	86.5	7.0	299	6 O9TTF9	O9ttf9 bos taurus
37	86	6.9	255	11 O9D3J3	O9d3j3 mus musculi
38	86	6.9	299	12 O84647	O84647 paramecium
39	86	6.9	706	5 O23600	O23600 caenorhabdi
40	86	6.9	911	11 O35A07	O35a07 mus musculi
41	85.5	6.9	795	5 O950Q2	O95uq2 toxoplasma
42	85	6.8	282	4 O9BSA1	O9bsa1 homo sapien
43	85	6.8	289	16 O9A3K1	O9a3k1 caulobacter
44	85	6.8	413	11 O99NM1	O99nm1 mus musculi
45	85	6.8	1217	4 O9P2D0	O9p2d0 homo sapien

ALIGNMENTS

RESULT 1

O9MZV0 ID O9MZV0 PRELIMINARY; PRT; 294 AA.
AC O9MZV0;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Flt3 ligand.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20358731; PubMed=10902925;
RA Yang S., Sim G.K.;
RT "Molecular cloning of canine and feline flt3 ligand reveals high
RT degree of similarity to the human and mouse homologue but uniquely
RT long cytoplasmic domain."
RL DNA Seq. 11:163-166(2000).
DR EMBL; AF15148; AAF87088.1; -
DR InterPro; IPR004213; Flt3_lig.
DR Pfam; PFO2947; Flt3_lig; 1.
SQ SEQUENCE 294 AA; 32394 MW; 6859917A3B74ABCD CRC64;

Query Match 72.1%; Score 895.5; DB 6; Length 294;
Best Local Similarity 77.1%; Pred. No. 3.5e-80;
Matches 182; Conservative 12; Mismatches 35; Indels 7; Gaps 3;

OY 1 MTVLAPAWSPTTYLLILLSSGSGTQDCSFQHSPISSDPFAVIRRLSYLLQDYPVY 60
DB 1 MTVLAPAWSPTASLLILLSSGSGTQDCSFQHSPISSDPFAVIRRLSYLLQDYPVY 60
OY 61 ASNIQDERLCGILRLVLAQKMERLKTVAQSKMQLGLERYNTEIHFVTCACQPPPSCL 120
DB 61 ASNIQDDELCAFWRLVLAQKMERLKTVAQSKMQLGLERYNTEIHFVTCACQPPPSCL 120
OY 121 RFGVNTSRLLQETSEQLVALKFWITRONFSRCLQCCQPPDSSTLPPPSRPLEATAPT 180
DB 121 RFGVNTSRLLQETSEQLVALKFWITRONFSRCLQCCQPPDSSTLPPPSRPLEATAPT 180

Q9GKD9 PRELIMINARY; PRT; 274 AA.
ID Q9GKD9;
AC Q9GKD9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PF flt3 ligand isoform-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20570936; PubMed=11120823;
RA Mwangi W., Brown W.C., Palmer G.H.;
RT Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain
RT required for receptor binding and function using naturally occurring
RT ligand isoforms.
RL J. Immunol. 165:6966-6974(2000).
DR EMBL: AF282986; AAF93323.1; -
DR InterPro: IPR004213; Flt3_lig.
DR Pfam: PF02947; flt3_lig; 1.
SQ SEQUENCE 274 AA; 30372 MW; 725A7E77A95DA98B CRC64;
Query Match 60.1%; Score 746; DB 6; Length 274;
Best Local Similarity 69.6%; Pred. No. 1.8e-65;
Matches 156; Conservative 12; Mismatches 34; Indels 22; Gaps 3;
QY 1 MTVLAPAMSP--TTTLLLLSSGSGTQDCSFQHSPISSDFAVKIRELSDYLLQDPVT 59
DB 1 MTVLAPAMSPSTTLLLLSPGLGTPDCSFHSPISSTFAIKIGKLSKYLQDPVT 60
QY 60 VASNLQDEELCGLMRLVLAQRWMERLKTAVAGSKMOGLLEVRNTEIHFTKCAFPQPPSC 119
DB 61 VASNLQDDKICGAFWRLVLAQRWGRKLTAVAGSEMKELEDVTEIHFTVTSCAF----- 114
QY 120 LRFVQTNISRLQETSEQVVALKPWITR--QNFSCLELQCPDPSSTLPFPPWSRPRELTA 179
DB 115 -----ODTHQOLEALKPWITHRNFSRCLQLCCQPDSPPTLLPPSPGALGATSL 162
QY 180 TAPQPP---LLLLLLPVGLLLLAAMCLHWQTRRRTRPPQEG 220
DB 163 PGQSPLLLLLLLPVALLLATATWCLCRWRRRRRTTRYPGR 206
RESULT 6
Q9L104 PRELIMINARY; PRT; 172 AA.
ID Q9L104;
AC Q9L104;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
PF flt3 ligand, flt3 form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX McClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Bacon K.,
RA Mattson J., Tsai S., Luh J., Gutmares M.J., Mattei M.G., Rosnet O.,
RT Birnbaum D., Hannum C.;
RT "Flt3 ligand: expression, genomic organization, alternatively spliced
RT forms and processing.";
RT Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U44024; AAF93305.1; -
DR MGD: MGI:95560; Flt3l.
DR InterPro: IPR004213; Flt3_lig.
DR InterPro: IPR001230; Prenyl_site.
DR Pfam: PF02947; flt3_lig; 1.
DR PROSITE: PS00294; PRENYLATION; UNKNOWN_1.

SQ SEQUENCE 172 AA; 19465 MW; 04F0A010171E3B84 CRC64;
Query Match 48.5%; Score 602.5; DB 11; Length 172;
Best Local Similarity 72.6%; Pred. No. 1.5e-51;
Matches 122; Conservative 15; Mismatches 28; Indels 3; Gaps 2;
QY 1 MTVLAPAMSP--TTTLLLLSSGSGTQDCSFQHSPISSDFAVKIRELSDYLLQDPVT 59
DB 1 MTVLAPAMSPNSLLLLSPCLRGTPDCYFSHSPISNFKKFRRLTDHLKDPVT 60
QY 60 VASNLQDEELCGLMRLVLAQRWMERLKTAVAGSKMOGLLEVRNTEIHFTKCAFPQPPSC 119
DB 61 VAVNLQDEKCKALMSFLAQRWIEQLKTAVAGSKMQLLEVDNTEIHFTVTSCTFQPLPEC 120
QY 120 LRFVQTNISRLQETSEQVVALKPWITR--QNFSCLELQCPDPSSTLPFPPWSRPRELTA 165
DB 121 LRFVQTNISHLKDPCTQLLAKPCIGKACQNFSCLEVQCPDPRVSL 168
RESULT 7
Q8VCH4 PRELIMINARY; PRT; 169 AA.
ID Q8VCH4;
AC Q8VCH4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to FMS-like tyrosine kinase 3 ligand.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RA TISSUE=LIVER;
RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC019801; AAF19801.1; -
DR InterPro: IPR004213; Flt3_lig.
DR Pfam: PF02947; flt3_lig; 1.
DR KW Kinase.
SQ SEQUENCE 169 AA; 18986 MW; 5B4CA47D9724EFP2 CRC64;
Query Match 46.5%; Score 578; DB 11; Length 169;
Best Local Similarity 68.6%; Pred. No. 3.7e-49;
Matches 120; Conservative 14; Mismatches 29; Indels 12; Gaps 3;
QY 1 MTVLAPAMSP--TTTLLLLSSGSGTQDCSFQHSPISSDFAVKIRELSDYLLQDPVT 59
DB 1 MTVLAPAMSPNSLLLLSPCLRGTPDCYFSHSPISNFKKFRRLTDHLKDPVT 60
QY 60 VASNLQDEELCGLMRLVLAQRWMERLKTAVAGSKMOGLLEVRNTEIHFTKCAFPQPPSC 119
DB 61 VAVNLQDEKCKALMSFLAQRWIEQLKTAVAGSKMQLLEVDNTEIHFTVTSCTFQPLPEC 120
QY 120 LRFVQTNISRLQETSEQVVALKPWITR--QNFSCLELQCPDPSSTLPFPPWSRPRELTA 172
DB 121 LRFVQTNISHLKDPCTQLLAKPCIGKACQNFSCLE-----TPPCCQ 166
RESULT 8
Q9L6G8 PRELIMINARY; PRT; 579 AA.
ID Q9L6G8;
AC Q9L6G8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative extensin-like protein.
GN P0406H10.6 OR OJ1174_D05.5.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eupharbioideae; Oryzoae; Oryza.
NCBI_TaxID=4530;

```
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nippondare(GA3) genomic DNA, chromosome 1, PAC
   clone: P040610."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nippondare(GA3) genomic DNA, chromosome 1, BAC
   clone: OJ1174_D05."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP002524; BAB07956.1; -.
DR EMBL: AP003118; BAB33013.1; -.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR002965; P_rich_extensn.
DR Pfam: PF00560; LRR; 6.
DR PRINTS: PR01583; KV33CHANNEL.
DR SMART: SM00370; LRR; 5.
DR PROSITE: PS00030; RRM_RNP_1; UNKNOWN_1.
SQ SEQUENCE 579 AA; 62607 MW; 04457E18E7405AAF CRC64;

Query Match          9.1%; Score 112.5; DB 10; Length 579;
Best Local Similarity 23.7%; Pred. No. 0.013;
Matches 54; Conservative 28; Mismatches 69; Indels 77; Gaps 11;

QY 17 LLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDYLDQPYVYASNLODEELCGIMRL 76
   :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 244 ILIINTGLS-----SCLPEVGM-LREIVTF-----DYGFNLRLAGLPSA 282
   :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 77 VLAQRMERKITYAGSKMÖGLERVNTIEHFYTKCAFQ-----PPSCIRFY-----QT 125
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 283 VAGMRKVEQL-DVAHNLITGAIQAVCELPRLKNFTFAVNFPTGEPSCAHVPRYGDGR 341
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 126 NI--SRLLQETSEQLVALKFWITRONFSR---CLELOCOPSSRLPPMSRPLEATAP 179
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 342 NCLPNRAQKITLRQCAAF-----FAHPVVCACAFQCKPVPYALPPSPSPSP 391
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 180 TAPQPLLILLIPVGLLLAAMCLHMORTRRRTPRGPGEVPPVPS 227
   :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 392 PSPPPP-----SPPPSTSPSPSP 411
   :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 9
Q9GY11 PRELIMINARY; PRT; 668 AA.
AC Q9GY11;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Probable surface antigen p2.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIDLIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
   Oliver K.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL390114; CAC02038.2; -.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001611; LRR.
DR Pfam: PF00560; LRR; 6.
DR PRINTS: PR01217; PRICHEXTENSIN.
DR SMART: SM00181; EGF; 1.

SQ SEQUENCE 668 AA; 70725 MW; CEB3EBCAABC490C94 CRC64;

Query Match          8.4%; Score 104.5; DB 5; Length 668;
Best Local Similarity 26.6%; Pred. No. 0.093;
Matches 63; Conservative 20; Mismatches 77; Indels 77; Gaps 13;

QY 4 LAPAWSPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLDQPYVYASN 63
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 149 LPPWSSMNPNTOTLOVRLKLSGT-----LPADWS-SLKSLSNVLEDMPT----- 194
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 64 LÖDEELCGGLMRVLVAQRMERKITYAGSKMÖGLERVNTIEHFYTKCAFQPPP-----S 118
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 195 -----GL-----LPPEW-----GSLERIQQLVLRKIKLTGFLPQWSPMK 229
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 119 CLRFVQ---TNISRLQ-----ETSQVALKP-WITRONSRCLQCOCP 160
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 230 ALRFLTLDTGNTLSGTLPPQWSAMASVISLNEGTEVSGTLPPKWIWSRL-QTINLRRTK 288
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 161 DSSTLPPWSPR-----PLEATAPTAPQP-----LILLILPVGL--LLAAM 203
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 289 VSGTLPPWSSMGSILANQLSLTQVSGTLPPQWSMKKLTQLLLTPTLLSGTLPAEM 345
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 11
Q8VIM6 PRELIMINARY; PRT; 648 AA.
AC Q8VIM6;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Probable surface antigen p2.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIDLIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
   Oliver K.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL390114; CAC02017.2; -.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001611; LRR.
DR Pfam: PF00560; LRR; 7.
DR PRINTS: PR01217; PRICHEXTENSIN.
DR SMART: SM00181; EGF; 1.

SQ SEQUENCE 648 AA; 68470 MW; 8EB78AC101E01286 CRC64;

Query Match          8.3%; Score 102.5; DB 5; Length 648;
Best Local Similarity 26.6%; Pred. No. 0.14;
Matches 63; Conservative 20; Mismatches 77; Indels 77; Gaps 13;
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ID 08VIM6 PRELIMINARY: PRT: 1809 AA.
 AC 08VIM6:
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Stereocillin.
 GN STRC.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BAIB/C.
 RX MEDLINE=21547528; PubMed=11687802.
 RA Verly E., Masmoudi S., Zwaenepoel I., Leibovici M., Hutchin T.P.,
 RA Del Castillo I., Nouaille S., Blanchard S., Laine S., Popot J.L.,
 RA Moreno F., Mueller R.F., Petit C.;
 RT "Mutations in a new gene encoding a protein of the hair bundle cause
 RT non-syndromic deafness at the DFNB16 locus.";
 RL Nat. Genet. 29:345-349(2001).
 DR EMBL: AF375593; AAL35321.1; -.
 DR MGD: MGI:2153816; Strc.
 SQ SEQUENCE 1809 AA; 196404 MW; 012382C9E80EC825 CRC64;

Query Match 8.1%; Score 100.5; DB 11; Length 1809;
 Best Local Similarity 23.7%; Pred. No. 0.74;
 Matches 70; Conservative 25; Mismatches 93; Indels 107; Gaps 14;

QY 3 VLAPAWSPPTLYLL-----LLLL-----SSGLSGTQCSFQHSISSDFAVKIRE 47
 DB 168 VLAADMLPFLMILLBETRMQALVOLQPSVDPYTNATGLDG-----RE 208
 DB 48 LSDYLLQDY--PVTVASNLQDEE-LOGGLMRLV---LAQRMMERIKTV----- 89
 DB 209 PAVHFLQGLGLITPAGELGSEALMGGLRTVGAPLVAFQEGILRYHSHQDEVFSIM 268
 QY 90 -----AGSMQGLLERVNTETIEFVTK-----AFQPPSCLEFVQTNISRL 131
 DB 269 GQPEPDASGCGGNIQQLLGMGRNLSWDARALGFLSGSPPPALHCLSRGVP--L 326
 QY 132 QETSEOLVALKPMITRONSRCLELQCCOPDSSTLP-----PMSPPLE 175
 DB 327 PRASQPAHISF---KQRAIVEALCENHSGPEPPYSISNFYLLCOHIKPAIPAPRPP 383
 QY 176 AT--APTAPQPPDLLLLLPVGLLLAAWCLHMQRTRRTPRGEQVP--PVPS 226
 DB 384 TTPRPPTTPQPPPTTQIP-----DTTQPPPTVPRPPPTTPQPPPS 426

RESULT 12
 ID 09N753 PRELIMINARY: PRT: 345 AA.
 AC 09N753:
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Probable surface antigen p2.
 GN LM12.08.
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ERIEDLIN;
 RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
 RA Oliver K.;
 RT Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AL390114; CAB98658.2; -.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR003592; LRR_out.
 DR Pfam: PF00560; LRR; 3.
 DR SMART: SM00370; LRR; 3.

SQ SEQUENCE 345 AA; 37530 MW; 06ECC850B1B54B70 CRC64;
 Query Match 7.9%; Score 98.5; DB 5; Length 345;
 Best Local Similarity 23.8%; Pred. No. 0.17;
 Matches 56; Conservative 21; Mismatches 57; Indels 101; Gaps 10;

QY 6 PMSPTTYLLILLSSGLST-----QDCSFQHSISSDFAVKIRELS 49
 DB 152 PEMGSMSTSLVNLRGICISCTLPQWGMKARSLOLQDCDLSGSPSSWSAI----- 205
 QY 50 DYLLQDVPVTVASNLQDEELCG-----GIMRLVQRMERIKTVAGSKQGLLERVNT 104
 DB 206 -----PMLASVSLKGNKFCGVCRTGIRLVLL--WTSRTSTRATA----- 245
 QY 105 IHFYTKAFQD--PPSCLEFVQTNISRLQETSEOLVALKPMITRONSRCLELQCCOPD 161
 DB 246 --WILRTVQGRPLPPLPPRQRPRTSLT-----PPLRGRPR 278
 QY 162 SSTLPPEPMSPPLENTAPAPQPLLL-----LLPVGLLLAAWCLHMQRTRR 212
 DB 279 LSRLPQALRRHRLN-----PQPLRRHRLNRPRLP-----QQTRR 313

RESULT 13
 ID 09DWH8 PRELIMINARY: PRT: 1240 AA.
 AC 09DWH8:
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Pr2.
 GN R2.
 OS Rat cytomegalovirus (strain Mastricht).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Muromegalovirus.
 OX NCBI_TaxID=79700;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MASTRICHT;
 RX MEDLINE=20366325; PubMed=10906222;
 RA Vink C., Beuken E., Bruggeman C.A.;
 RT "Complete DNA sequence of the rat cytomegalovirus genome.";
 RL J. Virol. 74:7656-7665(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MASTRICHT;
 RX MEDLINE=20473137; PubMed=11018281;
 RA Gruijthuisen Y.K., Beuken E., Bruggeman C.A., Vink C.;
 RT "Rat cytomegalovirus R89 is a highly conserved gene which expresses a
 RT spliced transcript.";
 RL Virus Res. 69:119-130(2000).
 DR EMBL: AF332689; AAF99111.1; -.
 SQ SEQUENCE 1240 AA; 125612 MW; 33B6C13DC6A272B0 CRC64;

Query Match 7.7%; Score 95.5; DB 12; Length 1240;
 Best Local Similarity 33.0%; Pred. No. 1.5;
 Matches 29; Conservative 8; Mismatches 18; Indels 33; Gaps 5;

QY 160 PDSSTL-----PPMSRPP--LEATAPAPQ--PLILLLLPVGLLLAA 201
 DB 1060 PDSSTAYTGEATTRSPATPEPRYRPLPCGVDSALPLAPQITTLSSLTPA----- 1112
 QY 202 AWCLHMQRTRRTRPRGEQVPVPVPSPOD 229
 DB 1113 -----QATRASRPETDAP--PTPAD 1132

RESULT 14
 ID 09C5T0 PRELIMINARY: PRT: 658 AA.
 AC 09C5T0:
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Receptor-like protein kinase 4.
GN RUK4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20575726; PubMed=11135117;
RA Du L., Chen Z.;
RT "Identification of genes encoding receptor-like protein kinases as
RT possible targets of pathogen- and salicylic acid-induced WRKY DNA-
RT binding proteins in Arabidopsis.";
RL Plant J. 24:837-847(2000).
DR EMBL: AF24705; AKK28315.1; -
DR InterPro: IPR002902; DUF26.
DR InterPro: IPR007119; Euk_pkinase.
DR InterPro: IPR002390; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF01657; DUF26. 2.
DR Pfam: PF00069; pkinase. 1.
DR ProDom: PD000001; Euk_pkinase. 1.
DR SMART: SM00220; S_TKC. 1.
DR SMART: SM00219; TYRKC. 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP. 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM. 1.
DR ATP-binding; Kinase; transferase.
SQ SEQUENCE 658 AA; 72991 MW; DCF9C5F1748F614 CRC64;

RESULT 15			
ID	017889	PRELIMINARY;	PRT; 1217 AA.
AC	017889;		
DT	01-JAN-1998 (TReMBLrel. 05, Created)		
DT	01-JAN-1998 (TReMBLrel. 05, Last sequence update)		
DT	01-MAR-2002 (TReMBLrel. 20, Last annotation update)		
DE	F54F12.1 protein.		
GN	F54F12.1.		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdillia; Rhabditioidea;		
CC	Rhabdillidae; Pelodicerinae; Caenorhabditis.		
OX	NCBI_TaxID=6239;		
LN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Barlow K.;		
RL	submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=99069613; PubMed=9851916;		
RT	note:		
RT	"genome sequence of the nematode C.elegans: A platform for investigating biology.";		
RT	Science 282;2012-2018(1998).		
EMBL	Z81548.CAB04464.1; -.		
DR	EMBL; Z81548.CAB04464.1; -.		

[illegible]

Search completed: November 24, 2002, 10:11:38
Job time : 31.2232 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 24, 2002, 10:02:26 ; Search time 31.7704 Seconds

(Without alignments)
985.632 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242
Sequence: 1 MVLAPAWSPPTYYLLLLLLL.....RPGEQVPVPSFDLLVEH 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SIDSz2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDSz2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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4: /SIDSz2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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21: /SIDSz2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDSz2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SIDSz2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	16	AA67541 Human flt-3 ligand.
2	1242	100.0	235	20	AA67769 Human flt-3 ligand.
3	1242	100.0	235	21	AA69719 Full length wild t
4	1242	100.0	235	22	AA620192 Human flt-3 ligand
5	1242	100.0	235	23	AA608129 Human flt-3 polype
6	1236	99.5	235	16	AA66175 Human S86/S109 flt
7	1236	99.5	235	22	AA620194 Human flt-3 ligand
8	1124	90.5	212	21	AA69721 Human flt-3 mutain
9	1114	89.7	209	19	AA69007 Human flt-3 recept
10	1114	89.7	209	21	AA69720 Mature wild type h

11	1110	89.4	209	21	AA69723 Human flt-3 mutain
12	1110	89.4	209	21	AA69726 Human flt-3 mutain
13	1110	89.4	209	21	AA69727 Human flt-3 mutain
14	1110	89.4	209	21	AA69729 Human flt-3 mutain
15	1108	89.2	209	21	AA69722 Human flt-3 mutain
16	1108	89.2	209	21	AA69724 Human flt-3 mutain
17	1107	89.1	209	21	AA69728 Human flt-3 mutain
18	1107	88.6	209	21	AA69725 Human flt-3 mutain
19	970	78.1	185	22	AA620195 Human flt-3 ligand
20	895.5	72.1	294	21	AA58204 Canine flt-3 ligand
21	894.5	72.0	291	21	AA58212 Canine flt-3 ligand
22	834	67.1	178	22	AA620193 Human flt-3 ligand
23	797.5	64.2	268	21	AA58206 Canine mature flt-
24	796.5	64.1	276	21	AA58207 Canine flt-3 ligand
25	791.5	63.7	265	21	AA58211 Canine mature flt-
26	768.5	61.9	231	16	AA67540 Mouse flt-3 ligand
27	768.5	61.9	231	20	AA67768 Murine flt-3 ligand
28	768.5	61.9	231	22	AA620186 Mouse flt-3 ligand
29	768	61.8	232	16	AA66177 Mouse M0T110/7118
30	764	61.5	232	22	AA620189 Mouse flt-3 ligand
31	745	60.0	150	19	AAW7930 Flt3 ligand FLR10C
32	745	60.0	150	19	AAW69054 Human flt-3 recept
33	740.5	59.6	377	19	AAW78124 Chimeric receptor
34	739	59.5	143	19	AAW77926 Flt3 ligand FLR3C
35	739	59.5	143	19	AAW69050 Human flt-3 recept
36	737.5	59.4	349	19	AAW83289 Human flt-3 ligand
37	737.5	59.4	349	19	AAW78005 Flt3L 1-139/1962b/
38	736.5	59.3	340	19	AAW83291 Human flt3 ligand
39	736.5	59.3	349	19	AAW83286 Human flt3 ligand
40	736.5	59.3	523	19	AAW78008 Trimeric flt3l-G-C
41	735	59.2	140	19	AAW77911 Human flt3 ligand
42	735	59.2	140	19	AAW69035 Human flt-3 recept
43	735	59.2	144	19	AAW77928 Flt3 ligand FLR4C
44	735	59.2	144	19	AAW69052 Human flt-3 recept
45	735	59.2	313	19	AAW83294 Human flt3 ligand

ALIGNMENTS

RESULT 1	
AA67541	
ID	AA67541 standard; Protein: 235 AA.
XX	
AC	AA67541;
XX	
AC	05-AUG-1995 (first entry)
XX	
DE	Human flt-3 ligand.
XX	
DE	Human flt-3 ligand.
XX	
KW	Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	Peptide
FT	Location/Qualifiers
FT	1..26
FT	/label= Sig-peptide
FT	/note= "signal peptide may extend to position 27"
FT	27..182
FT	/label= Domain
FT	/label= "Extracellular-domain
FT	/note= "extracellular domain may start at position 28"
FT	183..205
FT	/label= Domain
FT	/label= Transmembrane_domain
FT	206..235
FT	/label= Cytoplasmic_domain
PN	EP627487-A.
XX	
PD	07-DEC-1994.
XX	
PF	19-MAY-1994; 94EP-0303575.
XX	

PR 24-MAY-1993; 9305-0068394.
 PR 12-AUG-1993; 9305-0106463.
 PR 25-AUG-1993; 9305-0111758.
 PR 03-DEC-1993; 9305-0162407.
 PR 07-MAR-1994; 9405-0209502.
 PR 11-MAY-1994; 9405-0243545.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Beckmann MP, Lyman SD;
 XX
 DR WPI: 1995-008071/02.
 DR N-PSDB; AAQ79079.
 XX
 PT Isolated ligands for flt 3 receptors - useful for treating
 PT anaemia, AIDS and various cancers
 XX
 PS Disclosure; Page 29-30; 33pp; English.
 XX
 CC A human T-cell lambda-gli10 random primed cDNA library was
 CC screened with a fragment corresponding to the extracellular
 CC domain of mouse flt3 ligand (flt3-L) (nt 103-516 of AAQ79076)
 CC to isolate human flt3-L cDNA. Flt-3 stimulates progenitor and
 CC stem cells, and can be used e.g. in gene therapy protocols.
 XX
 SQ Sequence 235 AA:

 Query Match 100.0%; Score 1242; DB 16; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MTVALPAMSPPTYYLLLLSSGLSGTQDCSFQHSPISSDPAVKIRELSYLLQDYPTV 60
 DB 1 MTVALPAMSPPTYYLLLLSSGLSGTQDCSFQHSPISSDPAVKIRELSYLLQDYPTV 60
 QY 61 ASNIQDEBELCGGLMRLVLAQRMERLKTVAAGSKQGLLERVNTIHFVTKCAFOPPSCL 120
 DB 61 ASNIQDEBELCGGLMRLVLAQRMERLKTVAAGSKQGLLERVNTIHFVTKCAFOPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELOCOPDSSSTLPPWSRPLEATAPT 180
 DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELOCOPDSSSTLPPWSRPLEATAPT 180
 QY 181 APQPPLLILLPLVGLLLAAAWCLHWQTRRRTPRPGEQVPPVSPQDLLVEH 235
 DB 181 APQPPLLILLPLVGLLLAAAWCLHWQTRRRTPRPGEQVPPVSPQDLLVEH 235

 RESULT 2
 AAM67769
 ID AAM67769 standard; Protein: 235 AA.
 AC
 AC AAM67769;
 XX
 DT 25-MAR-1999 (first entry)
 XX
 DE Human flt3-L ligand.
 XX
 KW Antigen-specific peripheral immune tolerance; flt3-L ligand; flt3-L;
 KW immunogenic; autoimmune disease; organ transplantation; food allergy;
 KW tissue transplantation.
 XX
 OS Homo sapiens.
 OS
 PN MO9657655-A1.
 PD 23-DEC-1998.
 XX
 PF 12-JUN-1998; 98WO-US12085.
 XX
 PR 17-JUN-1997; 97US-0877421.
 XX
 PA (IMMV) IMMUNEX CORP.

XX
 PI Abbott NM, Mowat AM, Viney JL;
 XX
 DR WPI: 1999-070422/06.
 DR N-PSDB; AAV81506.
 XX
 PT Methods for initiating or enhancing antigen specific immune
 PT tolerance - by using murine or human flt3 ligand
 XX
 PS Claim 1; Page 14-15; 25pp; English.
 XX
 CC A method has been developed of initiating or enhancing: (i) an antigen-
 CC specific immune tolerance; or (ii) immunotolerance of a therapeutic
 CC immunogenic molecule by addition of a polypeptide, before, after or with
 CC the mucosal administration of an immunotolerising amount of the antigen
 CC or therapeutic molecule, respectively. The polypeptide is capable of
 CC binding the flt3 receptor and is: a) amino acids 28-x of murine flt3
 CC ligand (flt3-L), where x is an amino acid between 163-231; b) amino
 CC acids 28-y of human flt3-L, where y is an amino acid between 160-235;
 CC and c) a polypeptide that has at least 90% identity to the polypeptides
 CC of either (a) or (b). The method ameliorates the effects of autoimmune
 CC diseases, food allergies or organ or tissue rejection following
 CC transplantation. Administration of flt3-L allows lower doses of antigens
 CC to be used in vivo for mucosally administered antigens. The present
 CC sequence represents human flt3-L.
 XX
 SQ Sequence 235 AA:

 Query Match 100.0%; Score 1242; DB 20; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MTVALPAMSPPTYYLLLLSSGLSGTQDCSFQHSPISSDPAVKIRELSYLLQDYPTV 60
 DB 1 MTVALPAMSPPTYYLLLLSSGLSGTQDCSFQHSPISSDPAVKIRELSYLLQDYPTV 60
 QY 61 ASNIQDEBELCGGLMRLVLAQRMERLKTVAAGSKQGLLERVNTIHFVTKCAFOPPSCL 120
 DB 61 ASNIQDEBELCGGLMRLVLAQRMERLKTVAAGSKQGLLERVNTIHFVTKCAFOPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELOCOPDSSSTLPPWSRPLEATAPT 180
 DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELOCOPDSSSTLPPWSRPLEATAPT 180
 QY 181 APQPPLLILLPLVGLLLAAAWCLHWQTRRRTPRPGEQVPPVSPQDLLVEH 235
 DB 181 APQPPLLILLPLVGLLLAAAWCLHWQTRRRTPRPGEQVPPVSPQDLLVEH 235

 RESULT 3
 AAY69719
 ID AAY69719 standard; Protein: 235 AA.
 AC
 AC AAY69719;
 XX
 DT 05-JUL-2000 (first entry)
 XX
 DE Full length wild type human flt-3 protein.
 XX
 KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia.
 XX
 OS Homo sapiens.
 OS
 PN MO200001823-A2.
 PD 13-JAN-2000.
 XX

PF 25-JUN-1999; 99WO-US14296.
XX
PR 02-JUL-1998; 98US-0109100.
XX
PA (IMMUNEX CORP.
XX
PI Graddis TJ, McGrew JT;
XX
DR WPI: 2000-182115/16.
XX
N-PSDB; AAF59064.
PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions
PT contains amino acid substitutions at positions 8, 84, 118 or 122
XX
PS Claim 1; Page 72-73; 90pp: English.
XX
PS
CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (this sequence) or mature (AA169720) flt3-L
CC polypeptides. The flt3-L protein binds cell surface tyrosine kinase
CC receptors and regulate growth and differentiation of hematopoietic
CC progenitor cells. The flt3-L protein can be used to induce cellular
CC expansion (especially in vivo) or differentiation, e.g. in
CC hematopoietic, natural killer (NK) or dendritic cells, especially in the
CC presence of growth factors such as interleukins, colony stimulating
CC factors or protein kinases. The protein can also modulate, augment or
CC enhance a patient's immune response and can be used to treat an immune
CC disorder (e.g. allergy, autoimmunity or immunosuppression). The protein
CC may be used to treat a pathological condition e.g. myelodysplasia,
CC aplastic anemia, HIV infection, breast, small cell lung, testicular or
CC ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
CC leukemia.
XX
SQ Sequence 235 AA;
Query Match 100.0%; Score 1242; DB 21; Length 235;
Best Local Similarity 100.0%; Pred. No. 5e-109;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDPYTV 60
DB 1 MVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDPYTV 60
QY 61 ASNLQDEELCGGLMRVLVAQRMERLKTVAAGSKMGGLLERVNTLHFVTKCAFQPPPSCL 120
DB 61 ASNLQDEELCGGLMRVLVAQRMERLKTVAAGSKMGGLLERVNTLHFVTKCAFQPPPSCL 120
QY 121 RRVQTNISRLQETSEQLVALKPMWTRNFSRCLQLCCQPPSSLPPLPWSRPLEATAPT 180
DB 121 RRVQTNISRLQETSEQLVALKPMWTRNFSRCLQLCCQPPSSLPPLPWSRPLEATAPT 180
QY 181 AFQPLLLLLLPVGLLLAAAWCLHMORTRRRPRPGEQVPPVPSODLLVHH 235
DB 181 AFQPLLLLLLPVGLLLAAAWCLHMORTRRRPRPGEQVPPVPSODLLVHH 235
RESULT 4
AAB20192
ID AAB20192 standard; Protein: 235 AA.
XX
AC AAB20192;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human Flt-3 ligand.
XX
KM Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;
KM immunotherapy; therapy; tumour; cancer; melanoma; glioma;
KM lymphoma; autoimmune disease; infection; gene therapy.
XX
OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT Peptide 1..26
FT /label= Signal_peptide
FT Protein 27..235
FT /label= Mature_protein
FT Domain 27..182
FT /label= Extracellular_domain
FT Domain 183..205
FT /label= Transmembrane_domain
FT Domain 206..235
FT /label= Cytoplasmic_domain
PN WO200109303-A2.
XX
PD 08-FEB-2001.
XX
PF 31-JUL-2000; 2000WO-US20679.
XX
PR 30-JUL-1999; 99US-0146170.
XX
PA (VICA-) VICAL INC.
XX
PI Hermanson GS;
XX
DR WPI: 2001-123319/13.
DR N-PSDB; AAF30310.
XX
CC The present sequence is that of human Fms-like tyrosine kinase
CC (Flt-3 ligand). The invention is directed to enhancing the
CC immune response of a vertebrate to an antigen or a cytokine by
CC administering in vivo, into a tissue of a vertebrate, a Flt-3
CC ligand-encoding polynucleotide, and 1 or more antigen- or
CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
CC polynucleotide may encode the present full-length human Flt-3
CC ligand polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185,
CC or 27-235 of the ligand. The polynucleotides are incorporated
CC into the cells of the vertebrate in vivo, and a prophylactically
CC or therapeutically effective amount of Flt-3 ligand and 1 or more
CC antigens or cytokines is produced in vivo. Pharmaceutical
CC compositions comprising the polynucleotides are useful for
CC suppressing tumour growth in a mammal. The tumour is melanoma,
CC glioma or lymphoma, particularly B-cell lymphoma. They can also
CC be used for the prophylactic and/or therapeutic treatment of:
CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
CC and C in humans), parasitic (e.g. malaria) and fungal infections;
CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
CC Various other examples of these diseases are given in the
CC specification.
XX
SQ Sequence 235 AA;
Query Match 100.0%; Score 1242; DB 22; Length 235;
Best Local Similarity 100.0%; Pred. No. 5e-109;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDPYTV 60
DB 1 MVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDPYTV 60
QY 61 ASNLQDEELCGGLMRVLVAQRMERLKTVAAGSKMGGLLERVNTLHFVTKCAFQPPPSCL 120
DB 61 ASNLQDEELCGGLMRVLVAQRMERLKTVAAGSKMGGLLERVNTLHFVTKCAFQPPPSCL 120
QY 121 RRVQTNISRLQETSEQLVALKPMWTRNFSRCLQLCCQPPSSLPPLPWSRPLEATAPT 180
DB 121 RRVQTNISRLQETSEQLVALKPMWTRNFSRCLQLCCQPPSSLPPLPWSRPLEATAPT 180

Query Match 99.5%; Score 1236; DB 16; Length 235;
Best Local Similarity 99.6%; Pred. No. 1.8e-108;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGSGTGDCSFQHSPISSDFAVKIRLSYLLQDYPVTV 60
Db 1 MTVLAPAMSPPTTYLLLLSSGSGTGDCSFQHSPISSDFAVKIRLSYLLQDYPVTV 60
QY 61 ASNLQDEELCGGLMRVLVAQRMERLKTAVAGSKMGGLELVNTEIHFTVKCAFQPPSCL 120
Db 61 ASNLQDEELCGGLMRVLVAQRMERLKTAVAGSKMGGLELVNTEIHFTVKCAFQPPSCL 120
QY 121 RFVQNTISRLQETSSEQVVALKPKWITRONFSRCLELQCPDSSSTLPPWSPRPLEATAPT 180
Db 121 RFVQNTISRLQETSSEQVVALKPKWITRONFSRCLELQCPDSSSTLPPWSPRPLEATAPT 180
QY 181 APOPLLILLLPVGLLLAAAWCLHMORTRRTPRPGEOVPVPSPDILLVEH 235
Db 181 APOPLLILLLPVGLLLAAAWCLHMORTRRTPRPGEOVPVPSPDILLVEH 235

RESULT 7
AAB20194
ID AAB20194 standard; Protein; 235 AA.
AC AAB20194;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human Flt-3 ligand.
XX
KW Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;
KW immunotherapy; tumour; cancer; melanoma; glioma;
KW lymphoma; autoimmune disease; infection; gene therapy.
OS Homo sapiens.

FT Key Location/Qualifiers
FH Peptide 1..26 /Label= Signal_peptide
FT Protein 27..235 /Label= Mature_protein
FT Domain 27..182 /Label= Extracellular_domain
FT Domain 183..205 /Label= Transmembrane_domain
FT Domain 206..235 /Label= Cytoplasmic_domain

PN WO200109303-A2.
XX
XX 08-FEB-2001.
XX
XX 31-JUL-2000; 2000WO-US20679.
XX
XX 30-JUL-1999; 99US-0146170.
XX
XX (VICA-) VICAL INC.
XX
XX Hermanson GG;
XX
XX WPI; 2001-123319/13.
XX
XX N-PSDB; AAF30312.
XX
XX Immunogenic compositions comprising Flt-3 ligand encoding
XX polynucleotide and one or more antigen, or cytokine encoding
XX polynucleotides, useful for suppressing tumour growth and for
XX autoimmune diseases (e.g. rheumatoid arthritis) -
XX
XX Claim 2; Page 137-138; 149pp; English.
CC The present sequence is that of human Fms-like tyrosine kinase
CC (Flt-3 ligand). The invention is directed to enhancing the

CC immune response of a vertebrate to an antigen or a cytokine by
CC administering in vivo, into a tissue of a vertebrate, a Flt-3
CC ligand-encoding polynucleotide, and 1 or more antigen- or
CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
CC polynucleotide may encode the present full-length human Flt-3
CC ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235
CC of the Flt-3 ligand. The polynucleotides are incorporated into
CC the cells of the vertebrate in vivo, and a prophylactically or
CC therapeutically effective amount of Flt-3 ligand and 1 or more
CC antigens or cytokines is produced in vivo. Pharmaceutical
CC compositions comprising the polynucleotides are useful for
CC suppressing tumour growth in a mammal. The tumour is melanoma,
CC glioma or lymphoma, particularly B-cell lymphoma. They can also
CC be used for the prophylactic and/or therapeutic treatment of:
CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
CC and C in humans), parasitic (e.g. malaria) and fungal infections;
CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
CC Various other examples of these diseases are given in the
CC specification.

CC Sequence 235 AA:
SQ

Query Match 99.5%; Score 1236; DB 22; Length 235;
Best Local Similarity 99.6%; Pred. No. 1.8e-108;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGSGTGDCSFQHSPISSDFAVKIRLSYLLQDYPVTV 60
Db 1 MTVLAPAMSPPTTYLLLLSSGSGTGDCSFQHSPISSDFAVKIRLSYLLQDYPVTV 60
QY 61 ASNLQDEELCGGLMRVLVAQRMERLKTAVAGSKMGGLELVNTEIHFTVKCAFQPPSCL 120
Db 61 ASNLQDEELCGGLMRVLVAQRMERLKTAVAGSKMGGLELVNTEIHFTVKCAFQPPSCL 120
QY 121 RFVQNTISRLQETSSEQVVALKPKWITRONFSRCLELQCPDSSSTLPPWSPRPLEATAPT 180
Db 121 RFVQNTISRLQETSSEQVVALKPKWITRONFSRCLELQCPDSSSTLPPWSPRPLEATAPT 180
QY 181 APOPLLILLLPVGLLLAAAWCLHMORTRRTPRPGEOVPVPSPDILLVEH 235
Db 181 APOPLLILLLPVGLLLAAAWCLHMORTRRTPRPGEOVPVPSPDILLVEH 235

RESULT 8
AAV69721
ID AAV69721 standard; Protein; 212 AA.
AC AAV69721;
XX
XX 05-JUL-2000 (first entry)
XX
XX Human flt-3 mutein L-3H.
XX
XX
XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
XX neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
XX cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
XX cellular expansion; cellular differentiation; natural killer cell;
XX cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
XX myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
XX multiple myeloma; leukemia; mutein.

XX Homo sapiens.
XX Synthetic.
XX
XX WO200001823-A2.
XX
XX 13-JAN-2000.
XX
XX 25-JUN-1999; 99WO-US14296.
XX
XX 02-JUL-1998; 98US-0109100.

PA (IMMV) IMMUNEX CORP.
 XX
 PI Graddis TJ, McGrew JT;
 XX
 DR WPI; 2000-182115/16.
 XX
 PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
 XX
 PS Claim 4; Page 79-80; 90pp; English.
 XX
 XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AA69720) or mature (AA69720) flt3-L
 CC polypeptides. This sequence represents an example of the novel flt3-L
 CC ligands and comprises the L-3H mutant polypeptide. The flt3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
 CC be used to induce cellular expansion (especially in vivo) or
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins,
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or
 CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.
 XX
 XX Sequence 212 AA:
 SQ
 Query Match 90.5%; Score 1124; DB 21; Length 212;
 Best Local Similarity 100.0%; Pred. No. 5.9e-98;
 Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 25 SGTDCSFQHSPISSDFAVAKIRELSYLLQDYPVTVAASNLQDELCGGLMRVLQARWME 84
 DB 2 SGTDCSFQHSPISSDFAVAKIRELSYLLQDYPVTVAASNLQDELCGGLMRVLQARWME 61
 QY 85 RLKTIVAGSKMOGLLEHVNTEIHFTVCARQPPSCCLRFVQTNISRLQETSEQLVALKPMW 144
 DB 62 RLKTIVAGSKMOGLLEHVNTEIHFTVCARQPPSCCLRFVQTNISRLQETSEQLVALKPMW 121
 QY 145 ITRQNSRCLCLEOCQPDSSSTLPPWSPRPLEATAPAPQPLLILLLLPVGLLLAAAMC 204
 DB 122 ITRQNSRCLCLEOCQPDSSSTLPPWSPRPLEATAPAPQPLLILLLLPVGLLLAAAMC 181
 QY 205 LHMQRTRRRTPRPEGQVPVPSPODLLVEM 235
 DB 182 LHMQRTRRRTPRPEGQVPVPSPODLLVEM 212
 XX
 XX RESULT 9
 XX AAM69007
 XX ID AAM69007 standard; peptide; 209 AA.
 XX AC AAM69007;
 XX DT 01-OCT-1998 (first entry)
 XX DE Human flt-3 receptor agonist.
 XX DE Human flt-3 receptor agonist.
 XX DE Human; flt-3 receptor agonist; haematopoietic cell stimulation; cancer;
 KW bone marrow reconstruction; haematological disease; immune deficiency;
 KW drug-induced myelosuppression; renal dialysis; gene therapy; infection;
 KW congenital metabolic disease; neurological disease; therapy;
 KW dendritic cell production.
 XX
 XX Homo sapiens.
 XX
 XX PN WO9818923-A1.
 XX

PD 07-MAY-1998.
 XX
 EF 23-OCT-1997; 97NC-US18700.
 XX
 PR 25-OCT-1996; 96US-0030094.
 XX
 XX (SEAR) SEARLE & CC G D.
 XX
 PA Feng Y, McKearn JF, McWhorter CA, Minnerly JC, Munster NI;
 PI Staten NR, Streeter PR, Woulfe SL;
 XX
 XX WPI; 1998-272218/24.
 DR
 XX
 XX Rearranged flt-3 receptor agonists and nucleic acids encoding them
 PT used to stimulate production of haematopoietic and dendritic cells,
 PT for treatment of hematological diseases, bone marrow reconstitution
 PT and in gene therapy
 XX
 PS Disclosure; Page 9-10; 158pp; English.
 XX
 XX This sequence represents a rearranged human flt-3 receptor agonists of
 CC the invention. The agonists have a modified flt-3 ligand amino acid
 CC sequence. The agonists are used to stimulate production of haematopoietic
 CC cells in vivo (e.g. in a subject about to donate blood) or for ex vivo
 CC expansion for subsequent transplantation, e.g. to reconstitute bone
 CC marrow after chemotherapy, disease etc., or to treat haematological
 CC disease such as drug-induced myelosuppression, defects caused by
 CC infections, burns or renal dialysis. Optionally ex vivo expanded cells
 CC are transduced with a gene therapy vector for treating e.g. congenital
 CC metabolic diseases, immune deficiency, neurological disease, cancer and
 CC infections. The agonists can also be used in the treatment of tumours,
 CC infections and autoimmune disease, when administered optionally with an
 CC antigen. The agonist can also be used in the production of dendritic
 CC cells for use as an immunising adjuvant for treatment disorders including
 CC acquired immune deficiency syndrome. Compared with native ligands, the
 CC new agonists have better stimulatory activity, reduced side effects
 CC and/or better physical properties such as solubility, stability or refold
 CC efficiency. When used together with other stimulatory agents, the
 CC agonists provide a synergistic effect.
 XX
 XX Sequence 209 AA:
 SQ
 Query Match 89.7%; Score 1114; DB 19; Length 209;
 Best Local Similarity 100.0%; Pred. No. 5.1e-97;
 Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 27 TQDCSFQHSPISSDFAVAKIRELSYLLQDYPVTVAASNLQDELCGGLMRVLQARWME 86
 DB 1 TQDCSFQHSPISSDFAVAKIRELSYLLQDYPVTVAASNLQDELCGGLMRVLQARWME 60
 QY 87 KTVAGSKMOGLLEHVNTEIHFTVCARQPPSCCLRFVQTNISRLQETSEQLVALKPMW 146
 DB 61 KTVAGSKMOGLLEHVNTEIHFTVCARQPPSCCLRFVQTNISRLQETSEQLVALKPMW 120
 QY 147 RQNSRCLCLEOCQPDSSSTLPPWSPRPLEATAPAPQPLLILLLLPVGLLLAAAMC 206
 DB 121 RQNSRCLCLEOCQPDSSSTLPPWSPRPLEATAPAPQPLLILLLLPVGLLLAAAMC 180
 QY 207 WQRTTRRRTPRPEGQVPVPSPODLLVEM 235
 DB 181 WQRTTRRRTPRPEGQVPVPSPODLLVEM 209
 XX
 XX RESULT 10
 XX AAY69720
 XX ID AAY69720 standard; Protein; 209 AA.
 XX AC AAY69720;
 XX DT 05-JUL-2000 (first entry)
 XX DE Mature wild type human flt-3 protein.
 XX

Db 121 RQNFSCLELQCCPDSSSTLPPEWSPRPLEATAPAPQPELILLLLPVGLLLAAACGLH 180
QY 207 WQTRRRTPRGEQVPPVPSODLLVEH 235
181 WQTRRRTPRGEQVPPVPSODLLVEH 209

RESULT 12
AA69726
ID AAY69726 standard; Protein; 209 AA.
XX
AC AAY69726;
XX
DT 05-JUL-2000 (first entry)
XX
DE Human flt-3 muteln Q122R.
XX
KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; muteln.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001823-A2.
XX
PD 13-JAN-2000.
XX
PE 25-JUN-1999; 99WO-US14296.
PR 02-JUL-1998; 98US-0109100.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Graddis TJ, McGrew JT;
XX
DR WPI; 2000-182115/16.
XX
PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions
PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
XX
PS Claim 4; Page 88-89; 90pp; English.
XX
CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L
CC polypeptides. This sequence represents an example of the novel flt-3
CC ligands and comprises the Q122R mutant polypeptide. The flt3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.
XX
SQ Sequence 209 AA;
XX
Query Match 89.4%; Score 1110; DB 21; Length 209;
Best Local Similarity 99.5%; Pred. No. 1.2e-96;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAKIRELSDYLLQDYPVIVASNLQDEELCGGLMRLVLAQRMERL 86

Db 1 TQDCSFQHSPISSDFAKIRELSDYLLQDYPVIVASNLQDEELCGGLMRLVLAQRMERL 60
QY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCRLREVQINISLQETSQVALAKPWIT 146
Db 61 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCRLREVQINISLQETSQVALAKPWIT 120
QY 147 RQNFSCLELQCCPDSSSTLPPEWSPRPLEATAPAPQPELILLLLPVGLLLAAACGLH 206
Db 121 RQNFSCLELQCCPDSSSTLPPEWSPRPLEATAPAPQPELILLLLPVGLLLAAACGLH 180
QY 207 WQTRRRTPRGEQVPPVPSODLLVEH 235
Db 181 WQTRRRTPRGEQVPPVPSODLLVEH 209

RESULT 13
AA69727
ID AAY69727 standard; Protein; 209 AA.
XX
AC AAY69727;
XX
DT 05-JUL-2000 (first entry)
XX
DE Human flt-3 muteln L26F.
XX
KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; muteln.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001823-A2.
XX
PD 13-JAN-2000.
XX
PE 25-JUN-1999; 99WO-US14296.
PR 02-JUL-1998; 98US-0109100.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Graddis TJ, McGrew JT;
XX
DR WPI; 2000-182115/16.
XX
PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions
PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
XX
PS Claim 13; Page 82-83; 90pp; English.
XX
CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L
CC polypeptides. This sequence represents an example of the novel flt-3
CC ligands and comprises the L26F mutant polypeptide. The flt3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple

CC myeloma, neuroblastoma or acute leukemia.
 XX
 SQ Sequence 209 AA;
 Query Match 89.4%; Score 1110; DB 21; Length 209;
 Best Local Similarity 99.5%; Pred. No. 1.2e-96;
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 27 TODCSFOHSPISSDFAVKIRELSDYLLQDYPTVVASNLQDEELCGGLMRLVLAQRMERL 86
 DB 1 TODCSFOHSPISSDFAVKIRELSDYLLQDYPTVVASNLQDEELCGGLMRLVLAQRMERL 60
 QY 87 KTVAGSKMGLERVNTETHEFTKCAFOPPPSCLRFVQTNISRLQETSEQLVALKPWIT 146
 DB 61 KTVAGSKMGLERVNTETHEFTKCAFOPPPSCLRFVQTNISRLQETSEQLVALKPWIT 120
 QY 147 RQNFSCRLELQCCPDSSSTLPPMSPRPLEATAPAPQPPILLLLLPVGLLLAAACGLH 206
 DB 121 RQNFSCRLELQCCPDSSSTLPPMSPRPLEATAPAPQPPILLLLLPVGLLLAAACGLH 180
 QY 207 WQTRRRTRPRGEOVPVPVSPDILLVEH 235
 DB 181 WQTRRRTRPRGEOVPVPVSPDILLVEH 209

RESULT 14

AAy69729
 ID AAY69729 standard; Protein: 209 AA.
 XX
 AC AAY69729;
 DT 05-JUL-2000 (first entry)
 XX
 DE Human flt-3 mutein A64T.
 XX
 KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200001823-A2.
 XX
 PD 13-JAN-2000.
 XX
 PF 25-JUN-1999; 99WO-US14296.
 XX
 PR 02-JUL-1998; 98US-0109100.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Graddis TJ, McGrew JT;
 XX
 DR WPI: 2000-182115/16.
 XX
 PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
 XX
 PS Claim 13; Page 78-79; 90pp; English.
 XX
 CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L
 CC polypeptides. This sequence represents an example of the novel flt3-L
 CC ligands and comprises the 126F mutant polypeptide. The flt3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can

CC be used to induce cellular expansion (especially in vivo) or
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins,
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or
 CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.
 XX

SQ Sequence 209 AA;

Query Match 89.4%; Score 1110; DB 21; Length 209;
 Best Local Similarity 99.5%; Pred. No. 1.2e-96;
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFOHSPISSDFAVKIRELSDYLLQDYPTVVASNLQDEELCGGLMRLVLAQRMERL 86
 DB 1 TODCSFOHSPISSDFAVKIRELSDYLLQDYPTVVASNLQDEELCGGLMRLVLAQRMERL 60
 QY 87 KTVAGSKMGLERVNTETHEFTKCAFOPPPSCLRFVQTNISRLQETSEQLVALKPWIT 146
 DB 61 KTVAGSKMGLERVNTETHEFTKCAFOPPPSCLRFVQTNISRLQETSEQLVALKPWIT 120
 QY 147 RQNFSCRLELQCCPDSSSTLPPMSPRPLEATAPAPQPPILLLLLPVGLLLAAACGLH 206
 DB 121 RQNFSCRLELQCCPDSSSTLPPMSPRPLEATAPAPQPPILLLLLPVGLLLAAACGLH 180
 QY 207 WQTRRRTRPRGEOVPVPVSPDILLVEH 235
 DB 181 WQTRRRTRPRGEOVPVPVSPDILLVEH 209

RESULT 15

AAy69722
 ID AAY69722 standard; Protein: 209 AA.
 XX
 AC AAY69722;
 DT 05-JUL-2000 (first entry)
 XX
 DE Human flt-3 mutein H8Y.
 XX
 KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200001823-A2.
 XX
 PD 13-JAN-2000.
 XX
 PF 25-JUN-1999; 99WO-US14296.
 XX
 PR 02-JUL-1998; 98US-0109100.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Graddis TJ, McGrew JT;
 XX
 DR WPI: 2000-182115/16.
 XX
 PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
 XX

PS Claim 4; Page 81-82; 90pp; English.

The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AA669719) or mature (AA699720) flt3-L polypeptides. This sequence represents an example of the novel flt-3 ligands and comprises the 867 mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic progenitor cells. The flt3-L protein can be used to induce cellular expansion (especially in vivo) or differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins colony stimulating factors or protein kinases. The protein can also modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or immunosuppression). The protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, small cell lung, testicular or ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute leukemia.

SQ Sequence 209 AA;

Query Match	89.2%	Score 1108;	DB 21;	Length 209;
Best Local Similarity	99.5%;	Pred. No. 1.9e-96;		
Matches 208; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	27	TTQCSFHSPISSDPAAVYKIRELSYLLQDYPVTAASNLQDEELCGGLAMRLVLAORWMERL	86
Db	1	TTQCSFHSPISSDPAAVYKIRELSYLLQDYPVTAASNLQDEELCGGLAMRLVLAORWMERL	60
Qy	87	KTVASGSKMGGLERNYEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLALKRWIT	146
Db	61	KTVASGSKMGGLERNYEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLALKRWIT	120
Qy	147	RQNSRCLQELQCPDSSLTLPPEWSRPLEATAPAPROPPLILLLLPVGLLLAAACGH	206
Db	121	RQNSRCLQELQCPDSSLTLPPEWSRPLEATAPAPROPPLILLLLPVGLLLAAACGH	180
Qy	207	WQTRRRRTPRGEOVPPVPSQDILLVYEH	235
Db	181	WQTRRRRTPRGEOVPPVPSQDILLVYEH	209

Search completed: November 24, 2002, 10:10:12
Job time : 32.7704 secs

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OM protein - protein search, using sw model

Run on: November 24, 2002, 10:11:46 ; Search time 8.57296 Seconds

(without alignments)
429.309 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242
Sequence: 1 MTVLPAWSPRTYLLILL.....RPGGVPPVSPQDLLVEH 235

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications-AA:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	9	US-10-095-449-6
2	1242	100.0	235	10	US-09-448-378-1
3	1242	100.0	235	10	US-09-983-806-6
4	1242	100.0	235	10	US-09-904-536-1
5	1124	90.5	212	10	US-09-904-536-1
6	1114	89.7	209	10	US-09-904-536-18
7	1110	89.4	209	10	US-09-904-536-9
8	1110	89.4	209	10	US-09-904-536-12
9	1110	89.4	209	10	US-09-904-536-14
10	1110	89.4	209	10	US-09-904-536-17
11	1108	88.2	209	10	US-09-904-536-11
12	1108	88.2	209	10	US-09-904-536-15
13	1107	88.1	209	10	US-09-904-536-13
14	1106	88.0	209	10	US-09-904-536-13
15	1100	88.6	209	10	US-09-904-536-16
16	768.5	61.9	231	9	US-10-095-449-2
17	768.5	61.9	231	10	US-09-448-378-2
18	768.5	61.9	231	10	US-09-983-806-2
19	506.5	40.8	137	10	US-09-904-536-19

20	91.5	7.4	674	10	US-09-899-471-2	Sequence 2, Appl
21	91.5	7.4	698	10	US-09-899-471-5	Sequence 5, Appl
22	89.5	7.2	874	10	US-09-826-508-26	Sequence 26, Appl
23	89.5	7.2	941	9	US-09-793-139-47	Sequence 47, Appl
24	89.5	7.2	941	10	US-09-818-879-47	Sequence 47, Appl
25	89.5	7.2	941	10	US-09-211-7558-47	Sequence 47, Appl
26	87.5	7.0	415	10	US-09-826-212-6	Sequence 47, Appl
27	87.5	7.0	415	10	US-09-907-372-20	Sequence 20, Appl
28	87.5	7.0	479	10	US-09-935-727-8	Sequence 8, Appl
29	87.5	7.0	479	9	US-10-108-605-57	Sequence 57, Appl
30	87.5	7.0	570	9	US-09-991-496-104	Sequence 104, App
31	87.5	7.0	570	10	US-09-874-923-104	Sequence 104, App
32	85.5	6.9	519	10	US-09-925-300-1680	Sequence 1680, Ap
33	84.5	6.8	610	10	US-09-783-708-1	Sequence 1, Appl
34	84.5	6.8	913	10	US-09-223-490-4	Sequence 4, Appl
35	84.5	6.8	1134	9	US-10-001-873-50	Sequence 50, Appl
36	84	6.8	107	10	US-09-220-920-52	Sequence 52, Appl
37	84	6.8	220	10	US-09-220-920-26	Sequence 9, Appl
38	84	6.8	220	10	US-09-804-615-9	Sequence 9, Appl
39	84	6.8	1252	9	US-10-047-542-89	Sequence 89, Appl
40	82.5	6.6	334	10	US-09-953-342-24	Sequence 24, Appl
41	81.5	6.6	488	10	US-09-801-196-26	Sequence 26, Appl
42	81.5	6.6	865	9	US-09-957-995A-19	Sequence 19, Appl
43	81	6.5	428	9	US-10-047-542-60	Sequence 60, Appl
44	81	6.5	428	10	US-09-916-230-1	Sequence 1, Appl
45	81	6.5	574	9	US-10-047-542-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-10-095-449-6
Sequence 6, Application US/10095449
Patent No. US20020160004A1
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flic3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/095,449
FILING DATE: 13-Mar-2002
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/669,692
FILING DATE: 24-JUN-1996
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430

; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-095-449-6

Query Match 100.0%; Score 1242; DB 9; Length 235;
Best Local Similarity 100.0%; Pred. No. 2e-103;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLILLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTVY 60
DB 1 MTVALPAMSPPTTYLLILLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
QY 61 ASNLQDEELCGGLMRVLVAQRMERLKTAVGSKMOGLLEERVNTEIHFTVKCAFPQPPSCL 120
DB 61 ASNLQDEELCGGLMRVLVAQRMERLKTAVGSKMOGLLEERVNTEIHFTVKCAFPQPPSCL 120
QY 121 RFVQTNISRLQETSEQVVALKPWITRONFSRCLELQCCPDSTLPPWSPRLEATAPT 180
DB 121 RFVQTNISRLQETSEQVVALKPWITRONFSRCLELQCCPDSTLPPWSPRLEATAPT 180
QY 181 APQPLLILLLLPVGLLLAAAMCLHWQTRRRTPRREGVPPVPSQDILLVEH 235
DB 181 APQPLLILLLLPVGLLLAAAMCLHWQTRRRTPRREGVPPVPSQDILLVEH 235

RESULT 2
US-09-448-378-1
; Sequence 1, Application US/09448378
; Patent No. US20020034517A1
; GENERAL INFORMATION:
; APPLICANT: Brasel, Kenneth
; TITLE OF INVENTION: Dendritic Cell Stimulatory Factor
; FILE REFERENCE: 2836-D
; CURRENT APPLICATION NUMBER: US/09/448,378
; CURRENT FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent version 3.0
; SEQ ID NO 1
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-448-378-1

Query Match 100.0%; Score 1242; DB 10; Length 235;
Best Local Similarity 100.0%; Pred. No. 2e-103;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLILLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTVY 60
DB 1 MTVALPAMSPPTTYLLILLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
QY 61 ASNLQDEELCGGLMRVLVAQRMERLKTAVGSKMOGLLEERVNTEIHFTVKCAFPQPPSCL 120
DB 61 ASNLQDEELCGGLMRVLVAQRMERLKTAVGSKMOGLLEERVNTEIHFTVKCAFPQPPSCL 120
QY 121 RFVQTNISRLQETSEQVVALKPWITRONFSRCLELQCCPDSTLPPWSPRLEATAPT 180
DB 121 RFVQTNISRLQETSEQVVALKPWITRONFSRCLELQCCPDSTLPPWSPRLEATAPT 180
QY 181 APQPLLILLLLPVGLLLAAAMCLHWQTRRRTPRREGVPPVPSQDILLVEH 235
DB 181 APQPLLILLLLPVGLLLAAAMCLHWQTRRRTPRREGVPPVPSQDILLVEH 235

RESULT 3
US-09-983-806-6

; Sequence 6, Application US/09983806
; Patent No. US20020107365A1
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for Flt3/Flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft word, Version #5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/983,806
FILING DATE: 25-Oct-2001
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/444,626
FILING DATE: 19-MAY-1995
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-983-806-6

Query Match 100.0%; Score 1242; DB 10; Length 235;
Best Local Similarity 100.0%; Pred. No. 2e-103;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLILLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTVY 60
DB 1 MTVALPAMSPPTTYLLILLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
QY 61 ASNLQDEELCGGLMRVLVAQRMERLKTAVGSKMOGLLEERVNTEIHFTVKCAFPQPPSCL 120
DB 61 ASNLQDEELCGGLMRVLVAQRMERLKTAVGSKMOGLLEERVNTEIHFTVKCAFPQPPSCL 120
QY 121 RFVQTNISRLQETSEQVVALKPWITRONFSRCLELQCCPDSTLPPWSPRLEATAPT 180
DB 121 RFVQTNISRLQETSEQVVALKPWITRONFSRCLELQCCPDSTLPPWSPRLEATAPT 180
QY 181 APQPLLILLLLPVGLLLAAAMCLHWQTRRRTPRREGVPPVPSQDILLVEH 235
DB 181 APQPLLILLLLPVGLLLAAAMCLHWQTRRRTPRREGVPPVPSQDILLVEH 235

RESULT 4

```
US-09-904-536-1
; Sequence 1, Application US/09904536
; Patent No. US20020111475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-1
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Query Match          100.0%; Score 1242; DB 10; Length 235;
Best Local Similarity 100.0%; Pred. No. 2e-103;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MTVALPAMSPFTYLLLLLSGLSTGQDCSFQHSPISSDFAVKIRELSYLLQDYPVY 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MTVALPAMSPFTYLLLLLSGLSTGQDCSFQHSPISSDFAVKIRELSYLLQDYPVY 60

QY 61 ASNIQDEELCGGLMRVLVLAQRMWERLKTVAAGKQGLLEVRNTEIHFTVCARFQPPSCL 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 61 ASNIQDEELCGGLMRVLVLAQRMWERLKTVAAGKQGLLEVRNTEIHFTVCARFQPPSCL 120

QY 121 RFVQNTNSRLQETSBDVALKFWITRQNSRCLQLQCGDSSSTLPPWSPRLEATAPT 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 RFVQNTNSRLQETSBDVALKFWITRQNSRCLQLQCGDSSSTLPPWSPRLEATAPT 180

QY 181 APOPELLLLLLPVGLLLAAACLIHQWTRRRTPRGEQVPPVPSPODLLVEH 235
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 181 APOPELLLLLLPVGLLLAAACLIHQWTRRRTPRGEQVPPVPSPODLLVEH 235
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RESULT 5
US-09-904-536-10
; Sequence 10, Application US/09904536
; Patent No. US20020111475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 10
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-10
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Query Match          90.5%; Score 1124; DB 10; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.4e-93;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 25 SGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVYASNIQDEELCGGLMRVLVLAQRMWE 84
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 2 SGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVYASNIQDEELCGGLMRVLVLAQRMWE 84

QY 85 RLKTVAGSKMOGLLEVRNTEIHFTVCARFQPPSCLRFVQNTNSRLQETSBDVALKFW 144
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 85 RLKTVAGSKMOGLLEVRNTEIHFTVCARFQPPSCLRFVQNTNSRLQETSBDVALKFW 144
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```
QY 145 ITRQNSRCLQLQCGDSSSTLPPWSPRLEATAPTAPQPELLLLLPVGLLLAAAC 204
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 122 ITRQNSRCLQLQCGDSSSTLPPWSPRLEATAPTAPQPELLLLLPVGLLLAAAC 181

QY 205 LHMQTRRRTPRGEQVPPVPSPODLLVEH 235
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 182 LHMQTRRRTPRGEQVPPVPSPODLLVEH 212
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```
RESULT 6
US-09-904-536-18
; Sequence 18, Application US/09904536
; Patent No. US20020111475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 18
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-18
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Query Match          89.7%; Score 1114; DB 10; Length 209;
Best Local Similarity 100.0%; Pred. No. 4.1e-92;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPVYASNIQDEELCGGLMRVLVLAQRMWERL 86
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPVYASNIQDEELCGGLMRVLVLAQRMWERL 86

QY 87 KTVAGSKMOGLLEVRNTEIHFTVCARFQPPSCLRFVQNTNSRLQETSBDVALKFWIT 146
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 61 KTVAGSKMOGLLEVRNTEIHFTVCARFQPPSCLRFVQNTNSRLQETSBDVALKFWIT 120

QY 147 RQNSRCLQLQCGDSSSTLPPWSPRLEATAPTAPQPELLLLLPVGLLLAAACLIH 206
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 RQNSRCLQLQCGDSSSTLPPWSPRLEATAPTAPQPELLLLLPVGLLLAAACLIH 180

QY 207 WQTRRRTPRGEQVPPVPSPODLLVEH 235
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 181 WQTRRRTPRGEQVPPVPSPODLLVEH 209
```

```
RESULT 7
US-09-904-536-9
; Sequence 9, Application US/09904536
; Patent No. US20020111475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 9
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-9
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Query Match      89.4%; Score 1110; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 9.3e-92;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNIODEELCGGLMRLVLAQRMERL 86
   1 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNIODEELCGGLMRLVLAQRMERL 60
DB 1 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNIODEELCGGLMRLVLAQRMERL 60

QY 87 KTVAGSKMOGLLEERVNTEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 146
   61 KTVAGSKMOGLLEERVNTEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120
DB 61 KTVAGSKMOGLLEERVNTEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120

QY 147 RQNFSCLELQCCOPDSSSTLPWPSPRPLEATAPAPQPLLILLPVGILLAAACMLH 206
   121 RQNFSCLELQCCOPDSSSTLPWPSPRPLEATAPAPQPLLILLPVGILLAAACMLH 180
DB 121 RQNFSCLELQCCOPDSSSTLPWPSPRPLEATAPAPQPLLILLPVGILLAAACMLH 180

QY 207 WQTRRRTPRPGEOVPPVPSPODLLLVEH 235
   181 WQTRRRTPRPGEOVPPVPSPODLLLVEH 209
DB 181 WQTRRRTPRPGEOVPPVPSPODLLLVEH 209

RESULT 8
US-09-904-536-12
; Sequence 12, Application US/09904536
; Patent No. US2002011475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-12

Query Match      89.4%; Score 1110; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 9.3e-92;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNIODEELCGGLMRLVLAQRMERL 86
   1 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNIODEELCGGLMRLVLAQRMERL 60
DB 1 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNIODEELCGGLMRLVLAQRMERL 60

QY 87 KTVAGSKMOGLLEERVNTEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 146
   61 KTVAGSKMOGLLEERVNTEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120
DB 61 KTVAGSKMOGLLEERVNTEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120

QY 147 RQNFSCLELQCCOPDSSSTLPWPSPRPLEATAPAPQPLLILLPVGILLAAACMLH 206
   121 RQNFSCLELQCCOPDSSSTLPWPSPRPLEATAPAPQPLLILLPVGILLAAACMLH 180
DB 121 RQNFSCLELQCCOPDSSSTLPWPSPRPLEATAPAPQPLLILLPVGILLAAACMLH 180

QY 207 WQTRRRTPRPGEOVPPVPSPODLLLVEH 235
   181 WQTRRRTPRPGEOVPPVPSPODLLLVEH 209
DB 181 WQTRRRTPRPGEOVPPVPSPODLLLVEH 209

RESULT 9
US-09-904-536-14
; Sequence 14, Application US/09904536
; Patent No. US2002011475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
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; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-14

Query Match      89.4%; Score 1110; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 9.3e-92;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNIODEELCGGLMRLVLAQRMERL 86
   1 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNIODEELCGGLMRLVLAQRMERL 60
DB 1 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNIODEELCGGLMRLVLAQRMERL 60

QY 87 KTVAGSKMOGLLEERVNTEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 146
   61 KTVAGSKMOGLLEERVNTEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120
DB 61 KTVAGSKMOGLLEERVNTEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120

QY 147 RQNFSCLELQCCOPDSSSTLPWPSPRPLEATAPAPQPLLILLPVGILLAAACMLH 206
   121 RQNFSCLELQCCOPDSSSTLPWPSPRPLEATAPAPQPLLILLPVGILLAAACMLH 180
DB 121 RQNFSCLELQCCOPDSSSTLPWPSPRPLEATAPAPQPLLILLPVGILLAAACMLH 180

QY 207 WQTRRRTPRPGEOVPPVPSPODLLLVEH 235
   181 WQTRRRTPRPGEOVPPVPSPODLLLVEH 209
DB 181 WQTRRRTPRPGEOVPPVPSPODLLLVEH 209

RESULT 10
US-09-904-536-17
; Sequence 17, Application US/09904536
; Patent No. US2002011475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-17

Query Match      89.4%; Score 1110; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 9.3e-92;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNIODEELCGGLMRLVLAQRMERL 86
   1 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNIODEELCGGLMRLVLAQRMERL 60
DB 1 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNIODEELCGGLMRLVLAQRMERL 60

QY 87 KTVAGSKMOGLLEERVNTEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 146
   61 KTVAGSKMOGLLEERVNTEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120
DB 61 KTVAGSKMOGLLEERVNTEIHFTVKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120

QY 147 RQNFSCLELQCCOPDSSSTLPWPSPRPLEATAPAPQPLLILLPVGILLAAACMLH 206
   121 RQNFSCLELQCCOPDSSSTLPWPSPRPLEATAPAPQPLLILLPVGILLAAACMLH 180
DB 121 RQNFSCLELQCCOPDSSSTLPWPSPRPLEATAPAPQPLLILLPVGILLAAACMLH 180

QY 207 WQTRRRTPRPGEOVPPVPSPODLLLVEH 235
   181 WQTRRRTPRPGEOVPPVPSPODLLLVEH 209
DB 181 WQTRRRTPRPGEOVPPVPSPODLLLVEH 209
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RESULT 11
US-09-904-536-11
: Sequence 11, Application US/09904536
: Patent No. US2002011475A1
:
: GENERAL INFORMATION:
: APPLICANT: Gradaris, Thomas J.
: APPLICANT: McGrew, Jeffrey T.
: TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
: FILE REFERENCE: 03260..0028
: CURRENT APPLICATION NUMBER: US/09/904,536
: PRIOR FILING DATE: 2001-07-16
: PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
: PRIOR FILING DATE: 1999-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO. 11
:
: LENGTH: 209
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-904-536-11

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	Query Match	Score	DB	Length
	Local Similarity	99.5%	pred. No. 1, 4e-91	209
	Matches	Conservative	1; Mismatches	0; Indels
			0; Gaps	0;
Qy	27	100CSFQHSITSDFAVKTRFSDYLDQIPYVANSINQPELGSGIMRVYLAQRMMERL	86	
Db	1	100CSFQHSITSDFAVKTRFSDYLDQIPYVANSINQPELGSGIMRVYLAQRMMERL	60	
Qy	87	KTVAGSGMGLERVNTLHEVTKCAFQPPSCLRFVQVTINIRLQETSEQVALKRWIT	146	
Db	61	KTVAGSGMGLERVNTLHEVTKCAFQPPSCLRFVQVTINIRLQETSEQVALKRWIT	120	
Qy	147	RQNSFRLCLQCPDSSLPWPWSPPELEATPAQPPILLLLLLFVGLLLLAAMCWA	206	
Db	121	RQNSFRLCLQCPDSSLPWPWSPPELEATPAQPPILLLLLLFVGLLLLAAMCWA	180	
Qy	207	WQTRRRTPRPGQVPPVPSQDILLVHN	235	
Db	181	WQTRRRTPRPGQVPPVPSQDILLVHN	209	

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RESULT 12
US-09-904-536-15
Sequence 15 Application US/03904536
Patent NO. US20020111475A1
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904.536
CURRENT FILING DATE: 2001-07-16
PRIORITY APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIORITY FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-904-536-15

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	Query March	89.2%	Score 1108;	DB 10	Length 209;
	Best Local Similarity	99.5%	Pred. No. 1,4e-91;		
	Matches 208;	Conservative	0;	Mismatches 1;	Indels 0;
					Gaps 0;
OY	27	TQDSEFHSIISDPFAVKIRELSYDLYDYPYTVASINQDEELCGGLKRLVLAQRMERL	86		
Db	1	TQDSEFHSIISDPFAVKIRELSYDLYDYPYTVASINQDEELCGGLKRLVLAQRMERL	60		
OY	87	KTVAGSKMOGLLEVRNTEIHFVTKCAFQDPSCLEFVOTINISRLLOETSEDLAKRWIT	146		

Db	61	KTVAGSKMGILERNTEIHHVTCARPPSCIRFQUNISLLQENSEQVVALKPMIT	120
Qy	147	RQNSRCLELOCOPSSSTLPWPWSRPLEATAPAPQRPYLLLLPGLLLAAACLIH	206
Db	121	RQNSRCLELOCOPSSSTLPWPWSRPLEATAPAPQRPYLLLLPGLLLAAACLIH	180
Qy	207	WQRTRRTRPGEQVPPVPSQDILLVEH	235
Db	181	WQRTRRTRPGEQVPPVPSQDILLVEH	209

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RESULT 13
US-09-904-536-13
; Sequence 13, Application US/09904536
; Patent No. US20020111475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904.536
; PRIORITY FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIORITY FILING DATE: 1999-07-02
; NUMBER OF SEQ. ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-13

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	Query Match	89.1%	Score 1107	DB 10	Length 209
	Best Local Similarity	99.5%	Pred. No. 1.7e-91		
	Matches 209	Conservative	0	Mismatches 1	Indels 0
					Gaps 0
QY	27	TQDCSFQHPISSDPAVKIRELSVDYLLQDPYTVASNLQDEELCGLMRLVLAQRMWERL	86		
Db	1	TQDCSFQHSISSDPAVKIRELSVDYLPQDPYTVASNLQDEELCGLMRLVLAQRMWERL	60		
QY	87	KTVAGSMQGLLELVNETHFPYTKACAFQPPPCLEFQYQTNISRLQETSEQVALKPMIT	146		
Db	61	KTVAGSMQGLLELVNETHFPYTKACAFQPPPCLEFQYQTNISRLQETSEQVALKPMIT	120		
QY	147	RQNSRCLQLQCPDSDTLPPEWSPRELEATAPTAQPPDLLLLELVGILLAAAKCII	206		
Db	121	RQNSRCLQLQCPDSDTLPPEWSPRELEATAPTAQPPDLLLLELVGILLAAAKCII	180		
QY	207	WQTRRRKTPRRGQVPPVPSQDLLVEH	235		
Db	181	WQTRRRKTPRRGQVPPVPSQDLLVEH	209		

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/ RESULT 14
/ US-09-904-536-8
/ : Sequence 8, Application US/09904536
/ : Patent No. US2002011475A1
/ : GENERAL INFORMATION:
/ : APPLICANT: Graddis, Thomas J.
/ : APPLICANT: McGrew, Jeffrey T.
/ : TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
/ : FILE REFERENCE: 03260 0028
/ : CURRENT APPLICATION NUMBER: US/09/904,536
/ : CURRENT FILING DATE: 2001-07-16
/ : PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
/ : PRIOR FILING DATE: 1999-07-02
/ : NUMBER OF SEQ ID NOS: 20
/ : SOFTWARE: PatentIn Ver. 2.1
/ : SEQ ID NO 8
/ : LENGTH: 209
/ : TYPE: PRT
/ : ORGANISM: Homo sapiens
/

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